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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein

October 1, 2004, 16:31:28 Run on:

; Search time 55 Seconds (without alignments) 405.841 Million cell updates/sec

US-09-841-091B-20 391 1 LELYQGIKFBASQKKSAKER......NRIRSNSSAANLMAKKRVIR score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1990s:\* genesequ200s:\* genesequ2001s:\* genesequ2003s:\* genesequ2003s:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* geneseqp1980s:\* geneseqp20048:\* Database : 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	2 Aaw29102 Human pep	Aab66630 Human	7 Abb99727 Amino aci	S Abp81805 Human cho		4 Aaw29104 Enhanced	) Aar38890 Sequence	Aaw21567	3 Aab66618 Rat pancr	Abu62651 Rat	Aar40772 Sequ	Aab66625	3 Abu62653 Guinea pi	Aab66626 Guinea	Abu62654 Guinea	Aam15988 Peptide	Abb34984	7 Aam28487	Abb29805	Abb20392	•	l Aam55791 Human bra	Abg49816	3 Aam03723 Peptide	Aha17696
	ID	AAW29102	AAB66630	ABB99727	ABP81805	ABU62658	AAW29104	AAR38890	AAW21567	AAB66618	ABU62651	AAR40772	AAB66625	ABU62653	AAB66626	ABU62654	AAM15988	ABB34984	AAM28487	ABB29805	ABB20392	AAM68165	AAM55791	ABG49816	AAM03723	ABG37696
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	Score	380.5	380.5	380.5	380.5	380.5	353.5	316	316	316	316	289.5	289.5	289.5	289.5	289.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5
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Aaw21566 LETO rat Ada09865 Human rec			Human Human Human	Abb99728 Amino aci Abp81824 Human cho Abu62657 Human CCK	Ade82460 Human Pro Abp82236 G protein Aab02852 Human G p Aab02855 Human G p Aar41678 Human C p
AAW21566 ADA09865 AAD80751	AAR92293 AAR88462	AAR53264 AAR57738 AAW29101	AAB02846 AAB66629 ADA83728	ABB99728 ABP81824 ABU62657	ADE83460 ABP82236 AAB02852 AAB02855 AAR41678
363 6	381 2	4447	447 4 447 4 447 6	447 6 447 6 447 6	447 7 20 6 4447 3 4447 3 4447 2 4447
232 59.3 112 28.6		1112 28.6 1112 28.6 1112 28.6	28.6 28.6 28.6		112 28.6 107 27.4 106 27.1 106 27.1
26 23	30 0 6	1 8 8 8 1 8 8 8 1 8 8 8	35 36 11 37	38 1. 39 1. 40 1.	41 17: 443 11( 454 10(

## ALIGNMENTS

cholecystokinin; CCK; peptide hormone receptor; PHR; neuropeptide; mutant; messenger signal; agonist; antagonist; human; treatment; tumour; gastrointestinal disorder; central nervous system disorder; neurotoxin; substitution; enhanced receptor; hypoglyceamia. Human peptide hormone cholecystokinin (CCK) receptor A. AAW29102 standard; protein; 428 AA (first entry) 11-FEB-1998 AAW29102; RESULT 1 AAW29102 

Homo sapiens.

/note= "Glu at this position can be substituted to Gln (AAW29104)" Location/Qualifiers Key Misc-difference 138

303. .306 // /note= "These aminoacids can be substituted by His, Val, Misc-difference

Ser, Ala (AAW29104)

WO9721731-A1

19-JUN-1997.

96WO-US019958 11-DEC-1996; 95US-00570157. 11-DEC-1995; 03-SEP-1996; (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

Kopin AS, Beinborn M;

WPI; 1997-332726/30.

the Assay for peptide hormone receptor ligand using mutant forms of the receptors - where changes in second messenger signalling activity indicate that a compound is an agonist.

Disclosure; Page 54-55; 88pp; English.

This is the human peptide hormone cholecystokinin (hCCK) receptor A. A mutant form of this receptor can be created by substitution of certain

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a movel method for determining whether a candidate compound is an agonist or an antagonist of a peptide hormone receptor (FHR). The candidate compound is an agonist or an antagonist of a peptide hormone receptor (FHR). The candidate compound is exposed to the mutant form of the PHR that has the ability to compound is exposed to the mutant form of the PHR that has the ability to amplify the activity of an agonist as compared to the corresponding wild-type receptor. A change in the second messenger signalling activity of the enhanced receptor can be measured to indicate whether the candidate compound is an agonist or an antagonist. The agonists and antagonists can be used for treating or preventing disorders involving PHRs. They can be used for treating tumours, gastrointestinal disorders, central nervous system disorders of appetite regulatory systems, anxiety or panic, withdrawal consponse produced by chronic treatment or abuse of drugs or alcohol, response produced by chronic treatment or abuse of drugs or alcohol, injury, poisoning by neurotoxins, infertility, adenomas, obesity or diabetes. The use of the mutant PHRs provides for the more sensitive
                                                                                                                                                                                                                                                                                                                                                                                                              234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
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                                                                                                                                                                                                                                                                                                                    Score 380.5; DB 2; Length 428; Pred. No. 6.9e-40;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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92US-00861769.
92US-00928033.
                                                                                                                                                                                                                                                                                                                  97.3%;
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90...
The 19; Conservative
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                                                                                                                                                                                                                                                                                      Sequence 428 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-1992;
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CCK receptor proteins or fragments are useful for obtaining antibodies that can recognize CCK-expressing cells. The transformed eukaryotic cell lines are useful for studying the receptor in an environment similar to its native environment, e.g. in the context of studying the electrophysiology or binding properties of the receptor. The transformed prokaryotic or insect cell line is useful for expressing CCK receptor to produce large amounts of the receptor for immunological purposes or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel single cell biosensor, useful for detecting G protein-coupled receptor ligand in a sample, comprises cell overexpressing arrestin and oprotein-coupled receptor.
                                                                                                                                                                                                                                                                                          234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; GPCR; single cell biosensor; arrestin;
GPCR ligand; cholecystokinin-A receptor; CCK-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human cholecystokinin-A (CCK-A) receptor.
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                                                                                                                                                                                                    DB 4; Length 428;
                                                                                                                                                                                                                                      0; Indels
                                                                                                                              studying protein structure, e.g. crystallography
                                                                                                                                                                                                  Score 380.5; DB 4
Pred. No. 6.9e-40;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3F; 103pp; English.
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                                                                                                                                                                                                                                        Conservative
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N-PSDB; ABZ23129.
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Best Local Similarity
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                                                                                                                                                                  Sequence 428 AA;
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ABB99727
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The present invention relates to a cholecystokinin (CCK) receptor protein. The CCK receptor-encoding DNA molecule is useful for expressing and purifying CCK receptor protein to sequenceable-grade homogeneity. The

Disclosure; Fig 13; 82pp; English.

producing an homogeneity.

cholecystokinin (CCK) receptor-encoding DNA molecule, useful for lucing and purifying human CCK receptor protein to sequenceable-grade

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

WPI; 2001-136725/14

Wank SA;

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antibody against a particular GPCR, and in the production of specific
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  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular g protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                      test sample, and for detecting a compound that modulates GPCR internalisation in a test sample. It is useful for altering GPCR internalisation. It is also useful for detecting an inhibitor of
                                                                                                                 1;
                                                                                       6; Length 428;
                                                                                                                                                                                                                                                                                                                                                            Human cholecystokinin A receptor protein SEQ ID NO:94.
                                                                                     97.3%; Score 380.5; DB 6;
98.8%; Pred. No. 6.9e-40;
tive 0; Mismatches 0;
                                     acetylcholinesterase in a test sample
                                                                                                                                                                                                                                                                                  ABP81805 standard; protein; 428 AA
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                 Conservative
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                                                                                                  Local Similarity
nes 79; Conserv
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                                                              Sequence 428 AA;
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                                                                                       Query Match
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artibodies. The peptides and artibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antiganic peptides for GPCRs and antibodies are useful for dagnosing and designing drugs for GPCRs and antibodies are useful for dagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell corresponding of Alganosing and designing drugs for regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, afteroaclerosis, bacterial, fungal, protozoan or viral infections, osteoporosis, cancer, cardiomyopathy, chronic and acute disease, parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory constructory, expression, schizophrenia, dementia, mental retardation, memory constructory cancer, in which GPCRs are involved. The antibodies may be suced in immunosasays and immunodiagnosis. ABZ45531 to ABZ42869 encode GPCR proteins given in ABPB1675 to ABPB25018, which are used in the case of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA
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Matches 79; Conservative
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11-AUG-1992;
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cholecystokinn (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing CCK receptor by solubilising a biological preparation containing CCK receptor in 1% digitionin, applying the solubilised receptor preparation to a cationic exchange resin and purifying the eluate of the resin. The purified eluate is then added to an agarcse-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade purity. The CCK receptor protein of the invention may have immunomodulatory activity. The DMA molecule of the invention is useful for purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK proteins are useful for neuroendocrine modulation of the immune system, and for sequence represents the human cholecystokinin (CCKB) receptor protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholecystokinin; CCK; peptide hormone receptor; PHR; neuropeptide; mutant; messenger signal; agonist; antagonist; human; treatment; tumour; gastrointestinal disorder; central nervous system disorder; neurotoxin; substitution; enhanced receptor; hypoglycaemia, MH21/35.
                                                                                                                                                                                                                                                                                                                                                                                1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                Gaps
This invention relates to a novel isolated DNA molecule encoding a
                                                                                                                                                                                                                                                                                                                                              1,
                                                                                                                                                                                                                                                                                                         Score 380.5; DB 6; Length 428;
Pred. No. 6.9e-40;
0; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= M306A
/note= "wild type Met is replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= E1380
note= "wild type Glu is replaced by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "wild type Ala is replaced by His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "wild type Asn is replaced by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "wild type Leu is replaced by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhanced CCK-A/gastrin receptor MH21/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW29104 standard; protein; 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= A303H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= N304V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= L305S
                                                                                                                                                                                                                                                                                                          97.3%;
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96US-00718047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 304
                                                                                                                                                                                                                                                                          Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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03-SEP-1996;
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                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW29104;
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AAW29104
ID AAW2
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This mutant CCK-A receptor M21/35 is derived from the human peptide

CC hormone cholecystokinin (hCCK) receptor A. This enhanced receptor MH21/35

CC is created by the substitution of wild type Glu to Gln at amino acid

CD position 138 and wild type Ala, Asn, Leu, Met to His, Val, Ser, Ala

CR be used in a novel method for determining whether a candidate compound is

CC andidate compound is exposed to the mutant form of the PHR that has the

CC andidate compound is exposed to the mutant form of the PHR that has the

CC candidate compound is exposed to the mutant form of the PHR that has the

CC andidate compound is exposed to the mutant form of the PHR that has the

CC andidate compound is a agonist as compared to the

CC corresponding wild-type receptor. A change in the second messenger

CC signalling activity of the enhanced receptor can be measured to indicate

whether the candidate compound is an agonist or an antagonist. The

agonists and antagonists can be used for treating tumours, gastrointestinal

CC disorders, central hervous system disorders, neuroleptic disorders

CM depression, schizophrenia, disorders of appetite regulatory systems;

CM classifier of and head injury, poisoning by neurotoxins, infertility,

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, creatment or

abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

consistive detection of PHR agonists or antegonists. Note: The

CC the more sensitive detection of PHR agonists or antegonists.

CC the more sensitive detection of PHR agonists or antegonists.

CC provided in pages 54-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoded by the rat pancreatic cholecystokinin (CCK) A receptor \ensuremath{\mathsf{CDNA}} clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                     Assay for peptide hormone receptor ligand using mutant forms of the receptors - where changes in second messenger signalling activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholecystokinin receptor protein; CCK; gastrointestinal receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.4%; Score 353.5; DB 2; Length 428; Best Local Similarity 93.8%; Pred. No. 2e-36; Matches 75; Conservative 0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
/label= glycosylation site
/note= "see also AAs 28,39,205"
                  (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
                                                                                                                                                                               receptors - where changes in second mes
indicate that a compound is an agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR38890 standard; protein; 444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 NRIRSNSSAHVSAAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                               Claim 34; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 NRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Balaenoptera acutorostrata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                               Beinborn M;
                                                                                                        WPI; 1997-332726/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
07-FEB-1994
                                                               Kopin AS,
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The cholecystokinin (CCK)-A receptor gene of total length 10914 bp and coding for a protein having the present sequence was obtained from LETO rats and the sequences of all five exons, together with partial, flanking intron sequences were determined. Knowledge of the CCK-A receptor sequences is useful for genetic diagnosis of type II diabetes, e.g. by dientifying a deleted site present in the CCK-A receptor gene of type II diabetes patients. Also, expression of CCK-A receptor mRNA is lowered or absent in the tissue of a cholelithiasis patient. (Updated on 17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 308
                                                                                                                                                                                                       Genetic diagnosis of type II diabetes and cholelithiasis - by analysing cholecystokinin-A receptor expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 316; DB 2; Length 444; Pred. No. 1.4e-31; 8; Mismatches 4; Indels
                                                                                                                                                                            N-PSDB; AAT71575, AAT71576, AAT71577, AAT71579, AAT71579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholecystokinin; CCK receptor; purify
                                                                                                                                                                                                                                             Disclosure; Page 6-9; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat pancreatic CCKA receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 LNRIRSSSSAANLIAKKRVIR 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB66618 standard; protein; 444
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92US-00861769.
92US-00928033.
92US-00937609.
                                                                                                                 95JP-00178234.
                                                                                         95JP-00353546.
                                                                                                                                                                                                                                                                                                                                                                                                                         80.8%;
82.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.77
Matches 67; Conservative
                                                                                                                                         (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                      to standardise OS field)
                                                                                                                                                                   WPI; 1997-220430/20
               Rattus sp; (LETO).
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 444 AA;
                                       JP09065900-A.
                                                                                         29-DEC-1995;
                                                                                                                 20-JUN-1995;
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11-AUG-1992;
02-SEP-1992;
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                                                                11-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated DNA molecule encoding cholecystokinin receptor protein - are purified to isolate cholecystokinin receptor clones and produce anticholecystokinin receptor antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The rat pancreatic CCK A receptor cDNA clone encodes a protein with transmembrane domains, and homology with other G-protein receptro superfamily members. There are 4 potential sites of N-linked glycosylation. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diabetes mellitus, type 2 diabetes, CCK-A receptor, cholelithiasis, gallstone, diagnosis, deletion, mutation, LETO rat, OLETF rat, Otsuka Long-Evans Tokushima Fatty.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.8%; Score 316; DB 2; Length 444; 82.7%; Pred. No. 1.4e-31; ive 8; Mismatches 4; Indels
                                                  131. .152
/label= transmembrane III
173. .193
                                                                                                                            330. .350
/label= transmembrane VI
366. .389
/label= transmembrane VII
                         93. .119
/label= transmembrane II
                                                                                       /label≂ transmembrane IV
                                                                                                  226. .249
/label= transmembrane V
              transmembrane 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW21567 standard; protein; 444 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Fig 1; 110pp; English
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                                                                                                                                                                                                                                                                  92US-00831248.
92US-00861769.
92US-00928033.
92US-00937609.
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(first entry)
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Best Local Similarity 82.7
Matches 67; Conservative
 57. .82
/label=
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-272886/34.
                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ47667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 444 AA;
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                                                                                                                                                                                                                                                                                                          02-SEP-1992;
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06-AUG-1997
                                                                                                                                                                                                                   19-AUG-1993
                                                                                                                                                                                                                                                                                 01-APR-1992;
11-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                           Wank SA;
  Domain
                          Domain
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                                                                                                                            Domain
                                                                                                                                                     Domain
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note= "Asn is N-glycosylated"

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                                                                                                 The present invention relates to a cholecystokinin (CCK) receptor protein. The CCK receptor-encoding DNA molecule is useful for expressing and purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK receptor proteins or fragments are useful for obtaining antibodies that can recognize CCK-expressing calls. The transformed eukaryotic cell lines are useful for studying the receptor in an environment similar to list mative environment, e.g. in the context of studying the electrophysiology or binding properties of the receptor. The transformed prokaryotic or insect cell line is useful for expressing CCK receptor to produce large amounts of the receptor for immunological purposes or for
                                                                                                                                                                                                                                                                                                     249 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 308
                                                                                                                                                                                                                                                                                           28
                                        New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for producing and purifying human CCK receptor protein to sequenceable-grade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Peptide fragment obtained by CNBr cleavage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleavage or
                                                                                                                                                                                                                                                                                           1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; CCKA; cholecystokinin receptor; immunomodulator; receptor.
                                                                                                                                                                                                                                              Score 316; DB 4; Length 444;
Pred. No. 1.4e-31;
8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Peptide fragment obtained by CNBr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=, "Transmembrane domain III"
132. .158
                                                                                                                                                                                                          studying protein structure, e.g. crystallography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173. .193
/note= "Transmembrane domain IV"
205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Transmembrane domain II'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Transmembrane domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat pancreatic CCKA receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          ABU62651 standard; protein; 444 AA.
                                                                                                                                                                                                                                                                                                                                               309 LNRIRSSSSAANLIAKKRVIR 329
                                                                                                                                                                                                                                                                                                                                   59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                 Disclosure; Fig 1; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      digestion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         digestion"
                                                                                                                                                                                                                                                  82.7%;
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Best Local Similarity 82.7
Matches 67; Conservative
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/note= "T
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                   WPI; 2001-136725/14.
                                                                                                                                                                                                                                Sequence 444 AA;
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cholecystokinin (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing CCK receptor in 1$ digitonin, applying the solubilised receptor preparation to a cationic exchange resin and purifying the eluate of the resin. The purified eluate is then added to an agarose-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade purity. The DNA molecule of the invention may have immunomodulatory activity. The DNA molecule of the invention is useful for purifying CCK receptor protein to sequenceable-grade homogenelty. The CCK proteins are useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognise CCK-expressing cells. The present sequence represents the rat cholecystokinin (CCKA) receptor protein of
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                                                                               cleavage or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein, useful for neuroendocrine modulation of the immune system, for obtaining antibodies that can recognize CCK-expressing cells.
                                                                                                                                                          cleavage
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                                                                             'note= "Peptide fragment obtained by CNBr
                                                                                                                                                          'note= "Peptide fragment obtained by CNBr
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                                                                                                                                                                                                                                                                                        'note= "Transmembrane domain VII"
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82.7%; Pred. No. 1.4e-31;
ive 8; Mismatches 4;
                      "Transmembrane domain V"
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                                                                                                        digestion"
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92US-00861769.
92US-00928033.
92US-00937609.
93US-00029170.
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nes 67; Conservative
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N-PSDB; ACD62651.
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01-APR-1992;
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                                                                     Sequence encoded by the cholecystokinin (CCK) A receptor cDNA in guinea pig gallbladder and pancreas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The rat pancreatic CCK A receptor cDNA clone encodes a protein with transmembrane domains, and homology with other G-protein receptor superfamily members. There are 4 potential sites of N-linked glycosylation and sites for serine and threonine phosphorylation. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                    /label= Phosphorylation
/note= "see also AAs 256,274,292,300,414,416,419"
                                                                                             Cholecystokinin receptor protein; CCK; gastrointestinal receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%; Score 289.5; DB 2; Length 430;
                                                                                                                                            /label= glycosylation
/note= "see also AAs 12,24,190"
                                                                                                                                                           44. .67
/label= transmembrane domain I
                                                                                                                                                                                                                                                                                                            /label= phosphorylation
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                                                                                                                             Location/Qualifiers
              AAR40772 standard; protein; 430 AA.
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92US-00861769.
92US-00928033.
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/label= II
118. .137
/label= III
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/label= VII
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                                                                                                                                                                                                             158. .179
/label= IV
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/label= VI
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/label= V
                                              (revised)
(first entry)
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N-PSDB; AAQ47669.
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                                                                                                             Cavia porcellus
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Modified-site
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11-AUG-1992;
02-SEP-1992;
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                                              25-MAR-2003
07-FEB-1994
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                               AAR40772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~
                                                                                                             234 LELYQGIKFDAIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSGSN 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for
producing and purifying human CCK receptor protein to sequenceable-grade
                                                                              1 LELYQCIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
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                            Indels
                            10;
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79.3%; Pred. No. 3.3e-28;
tive 4; Mismatches 10
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                                                                                                                                                                                                                     294 RINRIRSSSSTANLMAKKRVIR 315
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                                                                                                                                                                                                                                                                                                                                                                               AAB66625 standard; protein; 430
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92US-00861769.
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92US-00937609.
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Best Local Similarity 79.3
Matches 65; Conservative
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AAB66625
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Query Match

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RESULT 13 ABU62653 ABU62653;

Cavia sp.

Domain

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Domain

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This invention relates to a novel isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing a CCK receptor in 1% digitonin, applying the solubilised receptor preparation to a cationic exchange resin and public by burlifying the eluate of the resin. The purified eluate is then added to an agarose-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade purity. The CCK receptor protein of the invention may have immunomodulatory activity. The DNA molecule of the invention may have immunomodulatory of activity. The DNA molecule of the invention is useful for purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK proteins are useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognise CCK-expressing cells. The present sequence represents the guinea pig cholecystokinin (CCKA) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                     New isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein, useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognize CCK-expressing cells.
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79.3%; Pred. No. 3.3e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guinea pig CCKA receptor protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB66626 standard; protein; 450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                            Example 3; Fig 6; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00831248.
92US-00861769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Conservative
                                      2003-503641/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-136725/14.
                                                   N-PSDB; ACD26215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6169173-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1992;
01-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-1992;
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   Wank SA;
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                                                                                                                                                                                                                            Guinea pig; CCKA; cholecystokinin receptor; immunomodulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Serine phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Serine phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Transmembrane domain III'
158. .179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Transmembrane domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Transmembrane domain IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Transmembrane domain I"
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/note= "Transmembrane domain V"
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/note= "Transmembrane domain V"
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/note≈ "Transmembrane domain V"
                                                                                                                                                                                                                                                                                                                                                                   note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                  note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
294 RINRIRSSSSTANLMAKKRVIR 315
                                                                                   ABU62653 standard; protein; 430 AA.
                                                                                                                                                                                          Guinea pig CCKA receptor protein.
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92US-00861769.
92US-00928033.
92US-00937609.
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                                                                                                                                                         (first entry)
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/note= "T
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                                                                                                                                                         13-SEP-2003
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02-SEP-1992;
10-MAR-1993;
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20-MAR-2003

07-FEB-1992; 01-APR-1992

Gaps 3;

10; Indels

93US-00029170

us-09-841-091b-20.rag

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WPI; 2003-503641/47.
                       (WANK/) WANK S A.
  10-MAR-1993;
                                             Wank SA;
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Matches
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                                                              The present invention relates to a cholecystokinin (CCK) receptor and purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK receptor protein to sequenceable-grade homogeneity. The CCK receptor proteins or fragments are useful for obtaining antibodies that can recognize CCK-expressing cells. The transformed eukaryotic cell lines are useful for studying the receptor in an environment similar to its native environment, e.g. in the context of studying the electrophysiology or binding properties of the receptor. The transformed prokaryotic or insect cell line is useful for expressing CCK receptor to produce large amounts of the receptor for immunological purposes or for
                                                                                                                                                                                                                                                                                   New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for producing and purifying human CCK receptor protein to sequenceable-grade
                                                                                                                                                                                                                                                                      1 LELYQGIKFBASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                           DB 4; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guinea pig; CCKA; cholecystokinin receptor; immunomodulator.
                                                                                                                                                                                                                                                4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transmembrane domain III
                                                                                                                                                                                studying protein structure, e.g. crystallography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Transmembrane domain IV"
                                                                                                                                                                                                                        74.0%; Score 289.5; DB 4.79.3%; Pred. No. 3.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Transmembrane domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Transmembrane domain V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guinea pig CCKA receptor protein #2.
                                                                                                                                                                                                                                                                                                                             cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                 58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                             ABU62654 standard; protein; 450 AA
                                            Disclosure; Fig 7; 82pp; English.
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92US-00861769.
92US-00928033.
92US-00937609.
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                                                                                                                                                                                                                                    Best Local Similarity 79.3
Matches 65; Conservative
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01-APR-1992;
11-AUG-1992;
02-SEP-1992;
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cholecystokinin (CCK) receptor protein. The invention also discloses a method for puritying a CCK receptor by solubilising a biological preparation containing CCK receptor in 1$ digitonin, applying the solubilised receptor preparation to a cationic exchange resin and puritying the eluate of the resin. The puritied eluate is then added to an agarose-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade purity. The CCK receptor protein of the invention may have immunomodulatory activity. The DNA molecule of the invention is useful for puritying CCK receptor protein to sequenceable-grade homogeneity. The CCK proteins are useful for neuroendocrine modulation of the immune system, and for betaining antibodies that can recognise CCK-expressing cells. The present sequence represents the guinea pig cholecystokinin (CCKA) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
New isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein, useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognize CCK-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                         This invention relates to a novel isolated DNA molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 289.5; DB 6;
79.3%; Pred. No. 3.5e-28;
iive 4; Mismatches 10;
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                                                                                                                                                   Disclosure, Fig 7; 83pp; English.
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Les 65; Conservative
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Job time : 59 secs
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234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
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Sequence 5, Appli
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Sequence 14, Appl
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Sequence 2
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391
1 LELYQGIKFEASQKKSAKER......NRIRSNSSAANLMAKKRVIR
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-076-170-31
US-08-076-170-31
US-08-076-170-6
US-08-076-510-6
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US-08-076-510-6
US-08-078-176-176-176
US-08-029-170-14
US-08-029-170-14
US-08-029-170-24
US-08-029-170-24
US-08-029-170-24
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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#1.30  Sequence 1, Appli Sequence 16, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6933, Appli Sequence 6933, Appli Sequence 6933, Appli Sequence 6933, Appli Sequence 111, Appli Sequence 1	59 293
Sequence Seq	SSSSRA 
SS 64 SS 88 88 88 88 88 88 88 88 88 88 88 88	TEROLST
30NIST 130 11.30 11.30	RPPRKLE         RPPRKLE
4-349-1 7-609-16 7-609-16 6-510-2 6-510-2 6-510-4 8-892A-5 6-510-4 7-276A-4 7-276A-4 7-276A-4 7-276A-4 7-276A-4 7-276A-4 7-2780 8-891A-2556 8-891A-2556 8-891A-2556 8-991A-2556 8-991A-2566 8-991A-256	LELYOGIKFEASOKKSAKERRPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA   -  -  -   -   -  -  -  -  -  -  -  -
15.2 1 US-09-004-349-1 15.2 1 US-07-937-609-16 15.3 3 US-08-029-170-16 15.3 4 US-09-04-349-2 15.3 1 US-07-937-609-2 15.3 1 US-07-937-609-2 15.3 1 US-09-076-510-4 15.3 1 US-07-937-609-2 15.3 3 US-08-029-170-27 15.3 4 US-09-076-510-4 15.3 1 US-08-08-08-08-08-08-08-08-08-08-08-08-08-	PSTTSSGKY             PSTTSSGKY
4 US 1 US 1 US 4 US 5 US 6 US 7 US 7 US 8 US 9 US 8 US	SAKERK        SAKERK
25.0 449 4 25.2 452 1 24.0 451 4 24.0 451 4 24.0 451 4 21.9 453 1 21.9 453 1 22.9 453 1 23.9 453 1 24.0 ANABER: DCP, DCP, DCP, DCP, DCP, DCP, DCP, DCP,	FEASOKE          FEASOKE
28 101.5 26.0 449 4 US-09-006 39 98.5 25.2 452 1 US-07-931 31 94 24.0 451 1 US-08-572 33 94 24.0 451 1 US-08-572 34 84.2 24.0 451 4 US-09-0073 35 84.5 21.9 453 1 US-09-075 36 85.5 21.9 453 1 US-09-075 39 85.5 21.9 453 1 US-09-075 39 85.5 21.9 453 1 US-09-075 39 85.5 21.9 453 1 US-09-075 42 65.5 16.9 453 1 US-09-075 43 65.5 16.9 453 1 US-09-075 44 65.5 16.9 453 4 US-09-075 45 63.5 16.2 253 4 US-09-03 46 63.5 16.2 253 4 US-09-03 47 63.5 16.2 253 4 US-09-03 48 65.5 16.8 437 4 US-09-03 48 65.5 16.8 437 4 US-09-03 49 85.5 21.9 453 1 US-09-03 40 85.5 16.9 12.4 4 US-09-03 40 85.5 16.2 253 4 US-09-03 40 63.5 16.2 253 4 US-09-13 40 63.5 16.2 10 US-09-03 40 63.5 16.2 10 U	JELYOGIKI
98.59 98 98.59 98.59 98.59 98.59 98.59 98.59 98.59 98.59 98.	234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
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                                                                                                                                                                                  US-08-029-170-31

Sequence 31, Application US/08029170

Sequence 31, Application US/08029170

Settent No. 6169173

GENERAL INFORMATION:

APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF

TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIPE: 22313-029
COUNTRY: USA
ZIP: 22313-029
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/029,170
CLASSIFLOATION NUMBER: US/08/029,170
FLING DATE: 19930310
CLASSIFLOATION NUMBER: US 07/937,609
FRIDRA APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FRIDRA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/981,733
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2e-39;
0;
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; Pred. No. 3.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADUNESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 NRIRSNSSAANLMAKKRVIR 313
                                     294 NRIRSNSSAANLMAKKRVIR 313
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60 NRIRSNSSAANLMAKKRVIR 79
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INFORMATION FOR SEQ ID NO: 31:
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98.8%;
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AMINO ACID
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Best Local Similarity 98.6
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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RESULT 3

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1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

GENERAL INPORMATION:

APPLICANT: KOpin, Alan S.

APPLICANT: Beinborn, Martin

TITLE OF INVENTION: ASSAY FOR AND USES OF PEPTIDE HORMONE

TITLE OF INVENTION: RECEPTOR AGONISTS

FILE REPERENCE: 00398/118002

CURRENT APPLICATION NUMBER: U3/09/004,349A

CURRENT FILING DATE: 1998-01-08

EARLIER APPLICATION NUMBER: 08/570,157

EARLIER FILING DATE: 1995-12-11

NUMBER OF SEQ ID NOS: 23
                                               GENERAL INFORMATION:

APPLICANT: KOPIN, Alan S.

APPLICANT: Beinborn, Martin

TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO

TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Blbing LLP

STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.3%; Score 380.5; DB 4
98.8%; Pred. No. 3.2e-39;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 00398/109002
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
PRIOR APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
CLASSIFICATION: 1N-PORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-004-349-5; Sequence 5, Application US/09004349A; Patent No. 6566080
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Sequence 5, Application US/09076510 Patent No. 6376198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.3
Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 617/428-020
TELEFAX: 617/438-7045
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not re.;
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-076-510-5
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                  CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110
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308 LNRIRSSSSAANLIAKKRVIR 328
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                                                                                                                                                                                                                                               1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
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7
                                                                                                                                    97.3%; Score 380.5; DB 4; Length 428;
llarity 98.8%; Pred. No. 3.2e-39;
Conservative 0; Mismatches 0; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08570157
Patent No. 5750353
GENERAL INFORMATION: Alan S. APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: AADDRESSEE: Fish & Richardson P.C. STREET: 225 Pranklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,157
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPERENCE/DOCKET NUMBER: 00398/109001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                           294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 ANRIRSNSSAANLMAKKRVIR 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 443 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                         ; ORGANISM: Homo sapiens
US-09-004-349-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                    Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
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                                                        TYPE: PRT
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              SEQ ID NO 5
                                       LENGTH:
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248 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.8%; Score 316; DB 4; Length 443; Best Local Similarity 82.7%; Pred. No. 3.6e-31; Matches 67; Conservative 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kopin, Alan S.
APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION ASSAY FOR AND USES OF PEPTIDE HORMONE
TITLE OF INVENTION: RECEPTOR AGONISTS
FILE REFERENCE: 00398/118002
CURRENT APPLICATION NUMBER: US/09/004,349A
                                                                                           APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
NUMBER OF SECUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,510
PILING DATE: 12 MAY 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 LNRIRSSSAANLIAKKRVIR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09004349A Patent No. 6566080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ANRIRSNSSAANLMAKKRVIR 79
US-09-076-510-6; Sequence 6, Application US/09076510; Patent No. 6376198
                                                                                                                                                                                                                                            E: Clark & Elbing LLP
176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 443 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/438-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        STREET: 176 F
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09-004-349-6
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Query Match
Best Local Similarity
Matches 67; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-029-170-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

80.8%; Score 316; DB 4; Length 443;
Best Local Similarity 82.7%; Pred. No. 3.6e-31;
Matches 67; Conservative 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/07937609
Patent No. 5319073
GENERAL INFORMATION:
APPLICANT: WANN, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
COMMESSPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 01-78E-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-78F-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-78G-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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THE PROPERTY OF ALL O
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
CURRENT FILING DATE: 1998-01-08
EARLIER APPLICATION NUMBER: 08/570,157
EARLIER FILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 LNRIRSSSSAANLIAKKRVIR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4444 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                ) ORGANISM: Rattus norvegicus
US-09-004-349-6
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US-07-937-609-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                        443
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                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                     1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                               Gaps
                                                               5
Score 316; DB 1; Length 444; Pred. No. 3.6e-31; 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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OPERATION OF THE CLOOS MASSICAL SECTION APPLICATION DATA:

APPLICATION NUMBER: US/08/029,170

FILING DATE: 19930310

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,609

FILING DATE: 02-SEP-1992

PRIOR APPLICATION NUMBER: US 07/928,033

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/928,033

FILING DATE: 11-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/861,769

FILING DATE: US 07/861,769

FILING DATE: US 07/861,769

FILING DATE: US 07/861,769

FILING NUMBER: US 07/831,248

FILING DATE: US 07/831,248

FILING NUMBER: US 07/831,248

FERERENCE/MOUNING NUMBER: US 07/831,248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-0299
COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           309 LNRIRSSSSAANLIAKKVIR 329
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-029-170-14; Sequence 14, Application US/08029170; Patent No. 6169173
                                                                                                                                                                                                                                          59 ANRIRSNSSAANLMAKKRVIR 79
            80.8%;
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TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 683-4109
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                     67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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, Patent No. 5994097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 430;
                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION:
CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: USA

ZIP: 22313-0299
COUNTY: USA
ZIP: 22313-0299
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILIN RClease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BEAT: Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION: 77.01936_030
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 289.5; 79.3%; Pred. No. 6.9
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                                                                       309 LNRIRSSSSAANLIAKKRVIR 329
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                                              59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                           Sequence 23, Application US/07937609
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US-08-919-624-3
; Sequence 3, Application US/08919624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LEWGTH: 430 amir-Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)836-9300
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Best Local Similarity 79.3
Matches 65; Conservative
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234 LELYQGIKFDAIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSSGSN 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
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APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 289.5; DB 2;
Pred. No. 6.9e-28;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,624
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-05
TELECOMMUNICATION INFORMATION:
TELEFACK: 415-85-055
TELEFAX: 415-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 430 amino acids
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Best Local Similarity 79.3
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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US-08-029-170-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-919-624-3
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254 LELYQGIKPDALQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSGSN 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 289.5; DB 1; Length 450; Pred. No. 7.3e-28; 4; Mismatches 10; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL: UNFORMATION:
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA-
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,170
FILING DATE: 19930310
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
                                                   CLASSIFICATION: 436
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INPORMATION:
NAME: BRNT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 RINRIRSSSTANLMAKKRVIR 335
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: guinea pig CCKA receptor
US-07-937-609-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 450 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 79.3
Matches 65, Conservative
    FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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; Sequence 24, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS: 29
; CORRESPONDENCE ADDRESS: Folgy & Larder STREET: 1800 Diagonal Road, Suite 500
; CITLE T. 1800 Diagonal Road, Suite 500
; CITLE T. 1800 Diagonal Road, Suite 500
; CONTROLL TO THE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 430;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PEDENCHISE
COMPUTER: PEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9e-28;
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
TVDP:
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 79.3
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-170-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-937-609-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08570157

Sequence 7, Application US/08570157

Patent No. 5750353

GENERAL INFORMATION:

APPLICANT: Relinborn, Martin

TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sish & Richardson P.C.
STREET: 225 Franklin Street

COUNTY: Boston

STATE: MA

COUNTY: Boston

STATE: MA

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: ELECTION DATA:

MEDIUM TYPE: 11-DEC-1995

CURRENT APPLICATION DATA:

PELIGATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,164

TELECHONE: TELECHONE: ATT/542-8906

TELECHONE: ATT/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.0%; Score 289.5; DB 3
Best Local Similarity 79.3%; Pred. No. 7.3e-28;
Matches 65; Conservative 4; Mismatches 10
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT', Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 RINRIRSSSSTANLMAKKRVIR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                   | IMMEDIATE SOURCE:
| CLONE: guinea pig CCKA receptor
| US-08-029-170-24
                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-570-157-7
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October 1, 2004, 16:37:50; Search time 130 Seconds (without alignments) 195.555 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1351062 seqs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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391
                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 20, Appl Sequence 20, Appl	Sequence 31, Appl	Sequence 94, Appl	Sequence 12, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 14, Appl	Sequence 23, Appl	Sequence 24, Appl	Sequence 35690, A	Sequence 7, Appli	Sequence 7, Appli
SUMMARIES	US-09-841-091B-20 US-10-251-703-20	US-09-443-745-31	US-10-225-567A-94	US-10-060-369-12	US-10-127-940-5	US-10-441-757-5	US-10-127-940-6	US-10-441-757-6	US-09-443-745-14	US-09-443-745-23	US-09-443-745-24	US-09-864-761-35690	US-10-127-940-7	US-10-441-757-7
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% Query Match Length DB	79	428	428	428	428	428	443	. 443	444	430	450	176	453	453
% Query Match	100.0	97.3	97.3	97.3	97.3	97.3	80.8	80.8	80.8	74.0	74.0	73.8	38.6	38.6
Score	391	380.5	380.5	380.5	380.5	380.5	316	316	316	289.5	289.5	288.5	151	151
Result No.	- 7	m	4	r.	9	7	<b>6</b> 0	o,	10	11	12	13	14	15

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17	112		447	0	o	29,
18	112		447	12	-09-87	78,
19	112		447	14	-10-15	10,
20	112		447	14	-10-22	13
21	112		447	15	-10-417-820A-78	78
22	112		447	16	US-10-723-955-78	78
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24	111.5		448	14	7	m
25	107	27.4	20	14	-10-22	8
26	106		447	12	- ï	H
27	106		447	12		13
28	106		447	15	US-10-417-820A-112	Ξ
29	106		447	15	4	13
30	106		447	16	US-10-723-955-112	Ξ
31	106		447	16	•	13
32	102		453	10	US-09-443-745-26	56,
33	5		449	14	US-10-127-940-1	٦,
34	101.5		449	14	US-10-441-757-1	Ä
35	98.5		452	10	US-09-443-745-16	16,
36	95		8	14	US-10-251-703-19	13
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38	94		451	14	US-10-441-757-2	'n
39	87		19	12	-091	13
40	87		13	14	US-10-251-703-13	Sequence 13, Appl
41	ഗ		453	10	US-09-443-745-27	27
42	85.5		453	14	US-10-127-940-4	4,
43	വ		453	14	-10-4	4
44	82		50	13		14
45	82		20	14	US-10-251-703-14	14
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RESULT 1	1 1	9				

Gaps
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 75

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US-10-225-567A-94
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Matches
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                                                                                APPLICANT: Milopulos, Athan
APPLICANT: Milopulos, Athan
APPLICANT: Covic, Lidija
TITLE OF INVENTION: G Protein Coupled Receptor Agonists and
TITLE OF INVENTION: Methods of Activating and Inhibiting G Protein Coupled
TITLE OF INVENTION: Receptors Using the Same
FILE REFERENCE: NEMC-215 CIP PAPLICATION NUMBER: US/10/251,703
CURRENT PILING DATE: 2002-09-20
FRIOR APPLICATION NUMBER: 09/841,091
PRIOR APPLICATION NUMBER: 60/198,993
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 20
LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPRKLELRQLSTGSSSRAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPRKLELRQLSTGSSSRAN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 391; DB 14; Length 79; 100.0%; Pred. No. 1e-37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09443745
Publication No. US20030055238A1
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence; ; OTHER INFORMATION: Peptide Sequence US-10-251-703-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
                    Sequence 20, Application US/10251703
Publication No. US20030148449A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RIRSNSSAANLMAKKRVIR 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.v
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US-10-251-703-20
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US-09-443-745-31
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GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: Licespan Biosciences

APPLICANT: Burmer, Glenna C.

APPLICANT: Rouse, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT FILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: Patentin version 3.1

SEQ ID NO 94

LENGTH 40-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Pred. No. 1.3e-35;
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-A0C-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INPORMATION:
NAME: BENTY, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
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98.8%;
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hes 79; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 79; Conserva
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LENGTH: 428 amino acids
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.8
Matches 79; Conservative
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Best Local Similarity 98.8
Matches 79; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
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US-10-127-940-6
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Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
PEPTIDE HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                            Score 380.5; DB 14; DC.2.
Pred. No. 1.38-35;
Transcripts 0; Indels
                           ; Sequence 12, Application US/10060369; Publication No. US20030139589A1; GENERAL INPORMATION: GENERAL INPORMATION: APPLICANT: Zastawny, Roman; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4; FILE REFERENCE: 2911-104; CURRENT APPLICATION UNMBER: US/10/60,369; CURRENT APPLICATION NUMBER: US 09/173565; PRIOR APPLICATION NUMBER: US 09/173565; RIDN FILING DATE: 1998-08-16; NUMBER OF SEQ ID NOS: 12; SEQ ID NO 12; SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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APPLICATION NUMBER: US/10/127,940
FILING DATE: 23.Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible SYSTEM: PC-DOS/MS-DOS SOFTWARE: PastSed version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10127940 Publication No. US20030180798A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         97.3%;
98.8%;
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INFORMATION FOR SEQ ID NO: 5:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                    US-10-060-369-12
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US-10-127-940-5
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234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
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                                                                                                                                                                                                                                                                                               1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA 59
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                   Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10441757

Sequence 5, Application US/10441757

Publication No. US2003019111441

GENERAL INPORMATION:
APPLICANT: Kopin, Alan S.
APPLICANT: Belinorn, Martin
TITLE OF INVENTION: RECEPTOR AGONISTS

FILE OF INVENTION: RECEPTOR AGONISTS

CURRENT APPLICATION NUMBER: US/10/441,757

CURRENT FILING DATE: 2003-05-20

PRIOR PELING DATE: 1998-01-08

PRIOR PELING DATE: 1998-01-08

PRIOR PELING DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030180798A1
GENERAL INFORMATION:
APPLICANT: Kopin, Alan S.
Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
PEPTIDE HORMONE RECEPTORS
                                                                                                                                                                                   97.3%; Score 380.5; DB 14; Length
98.8%; Pred. No. 1.3e-35;
tive 0; Mismatches 0; Indels
TYPE: amino acid
STRANDEDNESS: No. US20030180798A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                 294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 NRIKSNSSAANLMAKKRVIR 313
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7
                                                                                                               248 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGSR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KIRPPRKLELRQLSTGS-SSR 58
                                                                     1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
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                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CLOMING AND FUNCTIONAL EXPRESSION OF TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
82.7%; Pred. No. 4.3e-28;
ive 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/AA*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.8%; Score 316; DB 10; Best Local Similarity 82.7%; Pred. No. 4.3e-28; Matches 67; Conservative 8; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: 06/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: 08 07/937,609
FILING DATE: 02-SEP-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRICE APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-PEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                 308 LNRIRSSSSAANLIAKKRVIR 328
                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09443745 Publication No. US20030055238A1
                                                                                                                                                                59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
COUNTRY: USA
ZIP: 22113-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                         Stephen A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 444 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)683-4109
Best Local Similarity 82.7
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WANK, &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-443-745-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 316; DB 14; Length 443;
Pred. No. 4.3e-28;
8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KODIA. Alan S.
APPLICANT: KODIA. Alan S.
APPLICANT: Reinborn, Martin
TITLE OF INVENTION: ASSAY FOR AND USES OF PEPTIDE HORMONE
TITLE OF INVENTION: RECEPTOR AGONISTS
FILE REFERENCE: 00398/118002
CURRENT APPLICATION NUMBER: 08/10/441,757
CURRENT PELLIA DATE: 1998-01-08
PRIOR FILING DATE: 1998-01-08
PRIOR FILING DATE: 1998-01-08
PRIOR FILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: No. US20030180798A1 Relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/109002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
TELEFAX: 617/438-7045
                                                                                                                                                                                                                                   FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NDATA: US/09/076,510
FILING DATE: 12 MAY 1998
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.8%; Score 316;
                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
seQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-940-6
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Publication No. US20030191114A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 443 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.7%;
Matches 67; Conservative
                                                                       COMPUTER READABLE FORM:
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 443
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Query Match

249 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 308

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amino acid
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US-09-864-761-35690
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                            Sequence 23, Application US/09443745
Publication No. US20030055238A1
GENERAL INFORMATION:
APPLICATION NO. US20030055238A1
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 289.5; DB 10; Length
Pred. No. 4.9e-25;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CORRENT APPLICATION DATA:
PILING DATE: US/09/443,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: 08 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 RINRIRSSSTANLMAKKRVIR 315
                      309 LNRIRSSSSAANLIAKKRVIR 329
  59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIBM PC COMPUTER:
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79.3%;
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 65; Conserva
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                                                                                                                                                                                                                                                                                                                                                                        USA
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254 LELYQGIKFDAIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSSGSN 313
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Sequence 24, Application US/09443745

Publication No. US20030055238A1

GENERAL INFORMATION: CALONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/443,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.0%; Score 289.5; DB 10; Best Local Similarity 79.3%; Pred. No. 5.2e-25; Matches 65; Conservative 4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 40399/166 NIHD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
FILING DATE: 10-WAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-MG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAMME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 RINRIRSSSTANLMAKKRVIR 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703)836-9300
(703)683-4109
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                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
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262 ELYRGIQFEMDLNKEAKAHKNGVSTPTTIPSG--DEGDGCYIQVTKRRNTMEMSTLTPSV 319
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                                                                        1 RKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVI
                             KKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
PEPTIDE HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: No. US20030180798A1 Relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DMFA:
APPLICATION NUMBER: US/10/127,940
FILING DATE: 23-Apr-2002
CLASSIFICATION: vUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 SSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/10127940
Publication No. US20030180798A1
GENERAL INFORMATION:
APPLICANT: Kopin, Alan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 453 amino acids
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TELEFAX: 617/438-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.6%
Best Local Similarity 42.9%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                            79
                                                                                                                                            24
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                                                                                                                                                                                                                                                                                     RESULT 14
US-10-127-940-7
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                                                                                                                                                       APPLICANY: Hancal, David K.

APPLICANY: Chen, Wencheng
TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-65-26
PRIOR PELING DATE: 2000-65-36
PRIOR PELING DATE: 2000-69-37
PRIOR PELING DATE: 2000-69-37
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-10
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PRIOR PELING DATE: 2000-10-10
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Pred. No. 2.2e-25;
0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW271780.1, EVALUE 7.00e-07 P32238, EVALUE 2.00e-75
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WEXPRESSED IN HEART, SIGNAL = 2.5

WEXPRESSED IN HELLA, SIGNAL = 1.6

WEXPRESSED IN HELLA, SIGNAL = 1.6

WEXPRESSED IN BEAIN, SIGNAL = 2.1

WEXPRESSED IN LIVEA, SIGNAL = 3.5

WEXPRESSED IN LIVEA, SIGNAL = 1.6

WEXPRESSED IN BT474, SIGNAL = 1.6

WEXPRESSED IN ADULT LIVER, SIGNAL = 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35690
LENGTH: 176
Sequence 35690, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSED IN
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98.4%;
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                                                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 60; Conserv
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Gaps
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38.6%; Score 151; DB 14; Length 453;
Best Local Similarity 42.9%; Pred. No. 6.3e-09;
Matches 36; Conservative 15; Mismatches 25; Indels 8
Sequence 7, Application US/10441757
; Publication No. US20030191114A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: RECEPTOR AGONISTS
; TITLE OF INVENTION: RECEPTOR AGONISTS
; CURRENT APPLICATION UNMBER: US/10/441,757
; CURRENT PILING DATE: 2003-05-20
; PRIOR PILING DATE: 1998-01-08
; PRIOR PILING DATE: 1998-01-08
; PRIOR PILING DATE: 1998-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-441-757-7
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\*Search completed: October 1, 2004, 16:49:06 Job time: 131 secs

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OM protein - protein search, using sw model

October 1, 2004, 16:34:54; Search time 15 Seconds (without alignments) 506.609 Million cell updates/sec Run on:

US-09-841-091B-20 391 1 LELYQGIKFEASQKKSAKER.....NRIRSNSSAANLMAKKRVIR 79

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote	hypothetical prote	transcription fact	serine/threonine-s	lethal(3)malignant	hypothetical prote	hypothetical prote	hypothetical prote	finger protein XFO	structural protein	hypothetical prote	hypothetical prote	hypothetical prote	NGG1 protein - yea	vitellogenin 1 - m	sperm-specific pro
T00273	T29465	839356	860159	S57844	T29776	T13613	T48079	S65085	T30349	T18796	T19313	T16917	S41685	T43141	865494
~	N	N	~	N	~	~	~	~	N	~	~	~	~	~	7
1520	133	644	589	196	1046	1279	1401	232	555	300	333	419	702	1704	101
16.6	16.5	16.5	16.4	16.4	16.4	16.4	16.4	16.2	16.2	16.1	16.1	16.1	16.1	16.1	16.0
65	64.5	64.5	64	64	64	64	64	63.5	63.5	63	63	63	63	63	62.5
8	31	32	33	34	35	36	37	38	39	40	11	42	13	14	5

## ALIGNMENTS

RESULT 1

	JN0692
	cholecystokinin type A receptor - human
	C;Species: Homo sapiens (man)
	C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text change 20-Apr-2000
	C;Accession: JN0692; JN0590
	R;de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.
	Biochem. Biophys. Res. Commun. 194, 811-818, 1993
	A; Title: Molecular cloning, functional expression and chromosomal localization of the hun
	A; Reference number: JN0692; MUID:93343941; PMID:8343165
	A; Accession: JN0692
	A; Molecule type: mRNA
	A;Residues: 1-428 <dew></dew>
	A;Cross-references: GB:L19315; NID:g306595; PIDN:AAA02819.1; PID:g306596
	A; Experimental source: gallbladder
	R;Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.
	Biochem. Biophys. Res. Commun. 193, 204-211, 1993
	A;Title: Molecular cloning and functional expression of the human galibladder cholecystor
	A; Kelefence number: ON0590; MULD:93277552; PMLD:8503909
	A CACCESSION: UNDSAU
	Aistatus: nucleic acid sequence not snown
	A; Molecule type: DNA
	A;Residues: 1-428 <ulr></ulr>
	A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491
	A;Experimental source: gallbladder
	C; Comment: This protein has diverse physiological roles in the gastrointestinal system w
	ch, and secretion from gastric mucosal cells.
	C, Genetics:
	A;Gene: GDB;CCKAR
	A; Cross-references: GDB:141927; OMIM:118444
	A:Map position: 4pter-4qter
	C:Superfamily: neurokinin 1 receptor
	C; Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein; t
	F;40-67/Domain: transmembrane #status predicted <tml></tml>
	F;78-104/Domain: transmembrane #status predicted <tm2></tm2>
-	F;116-137/Domain: transmembrane #status predicted <tm3></tm3>
	F;158-178/Domain: transmembrane #status predicted <tm4></tm4>
	208-234/Domain: transmembrane
_	F;314-332/Domain: transmembrane #status predicted <tm6></tm6>
	350-369/Domain: transmembrane
_	F;10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted
_	
	by protein kinase A) #status prec
	Quely March Boot Incre Girlarity of 8% Drod N/C 60-13.
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	19; COMBETVALIVE U; MISMACCHES U; IMPER I; GADS

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Length 10; Indels

DB 2;

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Ribe Weerth, A.; Pisegna, J.R.; Wank, S.A.
Am. J. Physiol. 265, G1116-G1121, 1993
A; Filtle: Guinea pig gallbladder and pancreas possess identical CCK-A receptor subtypes: 1
A; Reference number: 151898; MUID:94106629; PMID:7916580
A; Reference number: 151898
A; Returner preliminary; translated from GB/EMBL/DDBJ
A; Rocule : preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-430 «RES»
A; Residues: 1-430 «RES»
A; Cross-references: GBS-68242; NID:g544723; PIDN:AAB29504.1; PID:g544724
C; Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 289.5; DB 2
Pred. No. 3.3e-23;
4; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 TGSS-SRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 RINRIRSSSSTANLMAKKRVIR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                      74.08;
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nes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 65; Conserv?
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A; Title: The seventh transmembrane domain of gastrin/CCK receptors contributes to non-pe
A; Reference number: PC2213; MUID:94296413; PMID:8024583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 366-389 <NAN>
C; Comment: This G-protein-coupled receptor is present in the gastrointestinal system, va
smooth muscle contraction of the gallbladder and stomach. It is capable of activating
ducing the subsequent release of intracellular calcium.
                                                                                                                                                                                       A42685

A401685

Cholecystokinin receptor type A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: A45685; JC4225; FC2213
R;Wank, S.A.; Harkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slattery, T. Proc. Natl. Acad. Sci. U.S.A. 99, 3125-3129, 1992
A;Tille: Purification, molecular cloning, and functional expression of the cholecy A;Accession: A42685
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aintrons: 53/1; 137/1; 224/2; 267/1
C; Superfamily: neurokinin 1 receptor
C; Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
F; 57-82/Domain: transmembrane #status predicted aTM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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cholecystokinin A receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
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A; Residues: 1-444 < WAN>

A; Residues: 1-444 < WAN>

A; Crose-references: GB: M88096; NID: 9203383; PIDN: AAA40899.1; PID: 9203384

A; Crose-references: pancreas

A; Note: sequence extracted from NCBI backbone (NCBIN: 93814, NCBIP: 93815)

R; Takata, Y.; Takiguchi, S.; Funakoshi, A.; Kono, A.

B; Takata, Y.; Takiguchi, S.; Funakoshi, A.; Kono, A.

A; Title: Gene structure of rat cholecystokinin type-A receptor.

A; Reference number: JC4225; MUID: 95382845; PMID: 7554260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;131-151/Domain: transmembrane #status predicted <TM3>F;173-193/Domain: transmembrane #status predicted <TM4>F;255-249/Domain: transmembrane #status predicted <TM5>F;330-348/Domain: transmembrane #status predicted <TM5>F;366-389/Domain: transmembrane #status predicted <TM6>F;366-389/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 1-223 <TAK>
A;Cross-references: DDBJ:D50608; NID:g1100752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 LNRIRSSSSAANLIAKKRVIR 329
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                                                             294 NRIRSNSSAANLMAKKRVIR 313
NRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Mantamadiotis, T.; Baldwin, G.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: PC2213
A; Status: preliminary
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Cholecystokinin-A receptor - mouse
Cibecises: Mus musculus (house mouse)
Cibecises: Mus musculus (house mouse)
Cibecises: Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Apr-2000
Cipacession: JC5599
Rilacourse, K.A.; Lay, J.M.; Swanberg, L.J.; Jenkins, C.; Samuelson, L.C.
Rilacourse, K.A.; Lay, J.M.; Swanberg, L.J.; Jenkins, C.; Samuelson, L.C.
A.Reference number: JC5599; MUID:97396148; PMID:9245702
A.Feference number: JC5599; MUID:97396148; PMID:9245702
A.Residues: acid sequence not shown
A.Rolecule type: DNA
A.Residues: 1-436 < LAC
A.Residues: 1-436 < LAC
A.Residues: Leanslation not complete
Cicoment: This receptor belongs to the seven transmembrane G-protein coupled receptor for dder contraction, and cholecystokinin inhibition of food intake.
Cicoment: This receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gastric CCK-A receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Bate: 14-411-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
C;Accession: S50150
R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
B;Ochim. Biophys. Acta 1219, 321-327, 1994
A;Fitle: Cloning and expression of the rabbit gastric CCK-A receptor.
A;Reference number: S50150
A;Reference number: S50150
A;Reference number: S50150
A;Retexus: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <REU>
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPST-----TSSGKYEDSDGCYL-KTRPPRKLELRQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%; Score 284.5; DB 2; 71.6%; Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;42-67/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 TSSSGGRINRIRSSGSAANLIAKKRVIR 321
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C;Accession: JQ1614
R;Nakata, H.; Matsui, T.; Ito, M.; Taniguchi, T.; Naribayashi, Y.; Azima, N.; Nakamura, P
Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992
A;Title: Cloning and characterization of gastrin receptor from ECL carcinoid tumor of Mas A;Reference number: JQ1614; MUID:92412082; PMID:1530611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Cross-references: GB:D12817; NID:g220646; PIDN:BAA02250.1; PID:g220647
C;Superfamily: neurokinin 1 receptor
C;Superfamily: neurokinin 1 receptor
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane #status predicted <TM1>
F;59-3D/Domain: transmembrane #status predicted <TM2>
F;37-109/Domain: transmembrane #status predicted <TM3>
F;132-180/Domain: transmembrane #status predicted <TM4>
F;216-243/Domain: transmembrane #status predicted <TM4>
F;216-243/Domain: transmembrane #status predicted <TM5>
F;34-357/Domain: transmembrane #status predicted <TM6>
F;380-398/Domain: transmembrane #status predicted <TM7>
F;380-398/Domain: transmembrane #status predicted <TM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Neurochem. 63, 1199-1106, 1994
A;Title: Identification and characterization of various cholecystokinin B receptor mRNA
A;Reference number: 848049, MUID:95016646; PMID:7931273
A;Accession: 848049
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-381 <JAG>
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F;7.30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;87,300,442/Binding site: phosphate (Ser) (covalent) #status predicted
F;87,124,205/Disulfide bonds: #status predicted
F;321/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrin receptor - multimammate rat (Mastomys natalensis)
C;Species: Mastomys natalensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Nov-1996 #text_change 20-Apr-2000
C;Accession: 548049
C;Accession: 548049
C;Accessionidt, A.; Popovici, T.; O'Donohue, M.; Roques, B.P.
J. Neurochem. 63, 1199-1206, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELYQGIKFEASQKKSAKER-----KTR----KTR
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                                                                                                                                                                                                                                                                                                    ; DB 2; Length 447; 0.00026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 PPRKLELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||: |:||:||:|
303 RSRLEMTTLTTPTPGPG---LASANQAKLLAKKRVVR 336
F;334-354/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.0%; Score 101.5; DB 2; 28.9%; Pred. No. 0.0035; ive 18; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                    28.6%; Score 112; 33.7%; Pred. No. 0
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Matches 34; Conservative
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Best Local Similarity
Matches 28; Conserv
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A, Molecule type: mRNA
A, Residues: 1-450 < NAK>
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Cipaces: 25-Feb-1994 #sequence revision 18-Nov-1994 #text_change 20-Jun-2000
Cipaces: 25-Feb-1994 #sequence revision 18-Nov-1994 #text_change 20-Jun-2000
Cipacession: A47430; JC1352; A46645; A48262
R.itc, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.; Nakata, H.
S.itc, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.; Nakata, H.
J. Biol. Chem. 268, 18300-18305, 1993
A;Title: Functional characterization of a human brain cholecystokinin-B receptor. A trog A;Reference number: A47430
A;Reference number: A47430
A;Residues: 1-47 atro-compared with conceptual translation
A;Molecule type: mRWA
A;Residues: 1-47 atro-compared with conceptual translation
A;Residues: 1-47 atro-compared from NCBI backbone (NCBIP:136448)
A;Residues: Bachi, A; Hughy, K; Wank, S.A.
B;Cores references: GBn D13305; NID:9305; PIDN:BAA02564.1; PID:9436040
A;Residues: Commun. 189, 296-303, 1992
A;Title: Molecular cloning of the human brain and gastric cholecystokinin receptor: Struence number: JC1352; MUID:93080572; PMID:1280419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: brain, gastric
b. Biol. Ch. M.; Beinborn, M.; McBride, B. W.; Lu, M.; Kolakowski Jr., L.F.; Kopin, A.S.
J. Biol. Chem. 268, 8164-8169, 1993
A; Title: The human brain cholecystokinin-B/gastrin receptor. Cloning and characterizatic
A; Reference number: A46645; MUID:93216795; PMID:7681836
A; Steatus: nucleic acid sequence not shown; not compared with conceptual translation
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C,Superfamily: neurokinin 1 receptor
C,Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone rece
F;57-81/Domain: transmembrane #status predicted <TM1>
F;91-116/Domain: transmembrane #status predicted <TM3>
F;131-150/Domain: transmembrane #status predicted <TM3>
F;171-192/Domain: transmembrane #status predicted <TM3>
F;171-192/Domain: transmembrane #status predicted <TM3>
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A,Note: sequence extracted from NCBI backbone (NCBIP:129156)
A,Note: sequence extracted from NCBI backbone (NCBIP:129156)
B,Song, I.; Brown, D.R., Wiltehire, R.N., Gantz, I.; Trent, J.M.; Yamada, T.
Proc. Natl. Acad. Sci. U.S.A. 90, 9085-9089, 1993
A,Title: The human gastrin/cholecystokinin type B receptor gene: alternative splice donc
                                                                                                                                                                                                                                                               RESULT 6
447430
gastrin/cholecystokinin receptor B, short splice form - human
N,Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
                                                                                                                                                                                                             1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA 59
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A;Residues: 1-447 <PIS>
A;Cross-references: GB:L04473; NID:g179997; PIDN:AAA35660.1; PID:g179998
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A;Residues: 1-447 <RES>
A;Cross-references: GB:L10822; NID:g406075; PIDN:AAC37528.1; PID:g406076
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A;Residues: 1-447 <LEE>
A;Cross-references: GB:L08112; NID:g306488; PIDN:AAA35657.1; PID:g306489
                                                                                                                               5
                                         Length 427;
                                                                                                                               10;
                                    68.5%; Score 268; DB 2; 71.2%; Pred. No. 6.4e-21; ive 11; Mismatches 10;
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A;Cross-references: GDB:136457; OMIM:118445
                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NRIRSNSSAANLMAKKRVIR 79
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A;Introns: 51/1; 135/1; 218/2; 271/1
                                    Query Match
Best Local Similarity 71.24
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A: Accession: JC1352
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Gaps

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Gastrin receptor - dog

Gispecies: Canis lupus familiaris (dog)

Cispecies: Canis lupus familiaris

Rikopin, A.S.; Lee, Y.M.; McBride, E.W.; Miller, L.J.; Lu, M.; Lin, H.Y.; Kolakowski Jr., Proc. Natl. Acas. Sci. U.S.A. 89, 3605-3609, 1992

A;Ttle: Expression cloning and characterization of the canine parietal cell gastrin recentation: S22817

A;Reference number: S32817

A;Status: Preliminary

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-453 <KOP>

A;Cross-references: EMBL:M87834; NID:g163956; PIDN:AAA30847.1; PID:g163957

C;Superfamily: neurokinin 1 receptor

C;Superfamily: neurokinin 1 receptor

C;Superfamily: neurokinin 1 receptor; transmembrane protein
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1359 <FUL>
A;Cross-references: EMBL:AP000196; PIDN:AAC24256.1; GSPDB:GN00019; CESP:B0041.7
A;Experimental source: strain Bristol N2; clone B0041
                                                                                                                                                                                                                                                                                                                                                                                                                           242 ELYLGIRFDSDSBSESQSRVRGQGGLPGGAAPGPVHQNGRCRPEAGLAG--EDGDGCYVQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C'Species: Caenorhabditis elegans
C'Date: 29-0c1-1999 #sequence_revision 29-0c1-1999 #text_change 29-0c1-1999
C'Accession: T34036
R'Fulton, R.; Wohldmann, P.
submitted to the RMBL Data Library, April 1997
A'Description: The sequence of C. elegans cosmid B0041.
                                                                                                                                                                                                                                                                                                                                                  -----KPSTTSSGKYEDSDGCYL-
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A;Introns: 12/2; 59/2; 248/2; 582/1; 675/1; 733/3; 966/2; 1044/2; 1310/3
                                                                                                                                                                             23.4%; Score 91.5; DB 2; Length 452; 29.1%; Pred. No. 0.04; ive 15; Mismatches 27; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.9%; Score 85.5; DB 2; Length 453; Best Local Similarity 28.3%; Pred. No. 0.18; Matches 28; Conservative 14; Mismatches 32; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.7%; Score 73; DB 2; Length 1359; Best Local Similarity 31.5%; Pred. No. 11; Matches 23; Conservative 12; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 LPRSRP--ALELSALTAPISGPGPGPR--PAQAKLLAKKRVVR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 --KTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : ||| |: | | | 303 RSRQTLELSALTAPTPGPGGGPRPYQ--AKLLAKKRVVR 339
        F;217-237/Domain: transmembrane #status predicted <TM5>F;339-359/Domain: transmembrane #status predicted <TM6>F;381-400/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 RPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein B0041.7 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                             2 ELYQGIKFEASQKKSAKER-------
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                       Local Similarity
es 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: B0041.7
                                                                                                                                                                         Query Match
Best Local S:
Matches 30
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Apr-2000
C;Accession: JC2459
R;Blandizzi, C.; Song, I.; Yamada, T.
Biochem. Biophys. Res. Commun. 202, 947-953, 1994
A;Title Molecular Coloning and structural analysis of the rabbit gastrin/CCKB receptor A;Reference number: JC2459; MUID:94324990; PMID:8048969
A;Accession: JC2459
A;Accession: JC2459
A;Accession: JC245 *BLA>
A;Residues: 1-452 *BLA>
A;Cross-references: GB:L31548; NID:9495663; PIDN:AAA31194.1; PID:9495665
C;Genetics:
A;Introns: 49/1; 133/1; 216/2; 273/1
C;Superfamily: neurokinin 1 receptor
C;Keywords: receptor; transmembrane #status predicted <TM1>F;85-104/Domain: transmembrane #status predicted <TM2>F;85-104/Domain: transmembrane #status predicted <TM3>F;169-187/Domain: transmembrane #status predicted <TM4>F;169-187/Domain: transmembrane #status predicted <TM4>F;1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A46195
A46195
A46195
A60lecystokinin B receptor subtype - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: A46195
Kyank, S.A.; Pisegna, J.R.; de Weerth, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992
A;Title: Brain and gastrointestinal cholecystokinin receptor family: structure and funct
A;Reference number: A46195; MUID:92409582; PMID:1528881
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                2 ELYQGIKFEASQKKSAKER------KPSTISSGKYEDSDGCYLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 BLYQGIKFEASQKKSAKER-------KPSTISSGKYEDSDGCYLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBIP:114084)
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: nucleic acid
A;Residues: 1-452 <MAN>
A;Cross-references: GB:M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%; Score 98.5; DB 2; Length 452;
30.0%; Pred. No. 0.0073;
tive 14; Mismatches 29; Indels 27;
                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                Length 381;
                                                                                                                                                                         231 L-PRSRLEMTTLTTPTPGPVPGPRPNQ--AKLLAKKRVVR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 L-PRSRLEMITLITPIPGPVPGPRPNQ--AKLLAKKRVVR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 TRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 TRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                              30; Conservative 14; Mismatches
                                                                                  A;Introns: 64/2; 147/2; 205/1
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.0%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: brain
                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                Query Match
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25; Gaps

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Indels 15;

Page

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A;Map position: 1
A;Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title: Genome sequence of the nematode C. elegans: a platform for investigating biology. Reference number: A7500, MUID:99069613; PMID:9851916
;Note: see websites genome.wustl.edu/gss/C elegans/ and www sanger ac.uk/Projects/C_elegins/.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-2823 <ST2>
A;Cross-references: GB:chr_1; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-2823 «M12>
A;Cross-references: EMBL:281125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
A;Experimental source: clone T22A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 QGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPR-----KL-ELRQLSTGS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein T22A3.8 [imported] - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
C,Accession: P87908 B87908
R,anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.3%; Score 71.5; DB 2; Length 2823; Best Local Similarity 34.2%; Pred. No. 34; Matches 27; Conservative 13; Mismatches 24; Indels 15.
       preliminary; translated from GB/EMBL/DDBJ
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Job time: 17 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2231 QGRIDKMARN--IAILKAK 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 SSRANRIRSNSSAANLMAK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
Molecule type: DNA
Residues: 1-2823 <STO>
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                                                                                                                                                                                                  C,Genetics:
A,Gene: CESP:T22A3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: F87908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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A; Cross-references: EMBL:M20926; NID:g164416; PIDN:AAA31016.1; PID:g164417
A; Tracemoto, K.; Efendic, S.; Mutt, V.; Makk, G.; Feistner, G.J.; Barchas, J.D.
Nature: 3.4, 4.76-478, 1986
A; Title: Pancreastatin, a novel pancreatic peptide that inhibits insulin secretion.
A; Reference number: A26419; MUID:87065127; PMID:3537810
A; Molecule type: protein
A; Residues: 256-304 c.TAT>
C; Comment: Pancreastatin may be a normal proteolysis product of endogenous porcine chrom C; Comment: Pancreastatin mature metabolism; glycoprotein C; Reywords: amidated carboxyl end; calcium binding; carbohydrate metabolism; glycoprotein F: 256-304/Product: pancreastatin #status experimental c.PCN>
F; 304/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                     A32284

Assistant A precursor - pig (fragment)

NyAlternate names: secretory protein;
NyAlternate names: secretory protein;
NyAlternate names: secretory protein;
NyContains: beta-granin; chromostatin; pancreastatin; parastatin; vasostatin
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 2: May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C;Accession: A32284; A26419

R;Iacangelo, A.L.; Fischer-Colbrie, R.; Koller, K.J.; Brownstein, M.J.; Eiden, L.E.
Bandocrinology 122, 23139-2341, 1988
A;Title: The sequence of porcine chromogranin A messenger RNA demonstrates chromogranin
A;Reference number: A32284; MUID:88196011; PMID:2834189
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A;Cross-references: EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
                                               8 KFEASQKKSAKERKPSTTSSGKYEDSD-GCYLKTRPPRKLELRQLSTGSSSRA---NRIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T23064; T25096
R;Barlow, K.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z19669
A;Accession: T23064
A;Accession: T23064
A;Accession: T23064
A;Accession: T23064
A;Accession: L2064
A;Accession: T23064
A;Accession: T23064
A;Accession: T23064
A;Accession: T23064
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18.3%; Score 71.5; DB 2; Length 446;
Best Local Similarity 32.5%; Pred. No. 5.4;
Matches 25; Conservative 10; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1996 A;Reference number: 219980 A;Accession: T25096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: clone H10E24 R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----STHPLASLPSKKR 185
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                                                                                                                                                                                                                              167 KSKKNKEKSVKKR 179
                                                                                                                                                       64 SNSSAANLMAKKR 76
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A; Molecule type: mRNA
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15;

24;

DB 2; Length 2823; Indels

Lipis Page Blank (uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 1, 2004, 16:33:33; Search time 9 Seconds (without alignments) 457.060 Million cell updates/sec

US-09-841-091B-20 391 1 LELYQGIKFEASQKKSAKER.....NRIRSNSSAANLMAKKRVIR 79 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P32238 homo sapien	12	Q63931 cavia porce		097772 oryctolagus			-				P46627 oryctolagus		Q9u7e0 caenorhabdi	P04404 sus scrofa	P27476 Baccharomyc	Q9z0e3 mus musculu						P28875 candida alb							P32494 saccharomyc		Q44342 agrobacteri	Q8f7k1 leptospira
SUMMARIES	EI .	CCKR HUMAN	CCKR_RAT	CCKR_CAVPO	CCKR_MOUSE	CCKR_RABIT	CCKR_XENLA	GASR_HUMAN	GASR_MOUSE	GASR_PRANA	GASR_RAT	GASR_BOVIN	GASR RABIT	GASR_CANFA	ATRX CAEEL	CMGA_PIG	NSR1_YEAST	AIRE MOUSE	KAPA_YEAST	ATRX_HUMAN	ATRX_PANTR	ATRX_PONPY	T2FA_YEAST	CZF1_CANAL	BTD_DROME	MBN DROME	Y232 HUMAN	SWA DROPS	RRSI CAEEL	STE7_CANAL	ADA3_YEAST	VIT1_FUNHE		IF2_LEPIN
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J	Query Match	97.3	80.8	74.0	72.8	70.3	38.6	28.6	26.3	26.0	25.2	24.2	23.4	21.9	18.7	18.3	17.6	17.1	16.9	16.9	16.9	16.9	16.8	16.5	16.5	16.4	16.4	16.2	16.1	16.1	16.1	16.1	16.0	16.0
	Score	380.5	316	289.5	284.5	275	151	112	103	101.5	98.5	94.5	91.5	85.5	73	71.5	69	67	99	99	99	99	65.5	64.5	64.5	64	64	63.5	63	63	63	63	62.5	62.5
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Q04621 mytilus edu P35269 homo sapien	Oguhi6 homo sapien Ogy2w1 homo sapien P87498 gallus gall	Q8bzx4 mus musculu P70056 xenopus lae	P05986 saccharomyc P14923 homo sapien P40815 salmonella	Q99020 mus musculu Q99729 homo sapien
PHI1_MYTED T2FA_HUMAN	DD20_HUMAN T150_HUMAN VIT1_CHICK	SFRC_MOUSE FXH1_XENLA	KAPC YEAST PLAK HUMAN T3RE SALTY	ROAA_MOUSE ROAA_HUMAN
7				
91 517	824 955 1912	494 518	398 743 990	331
15.7	15.6 15.6	15.5	15.3	15.2
61.5	61 61 61	60.5	000	59.5
34 35	36 37 38	33	4 4 4 4 5 6	44 45

## ALIGNMENTS

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TRANSMEM
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                                                RESULT 2
                                                                     CCKR_RAT
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REMEL; U23420; AAA91123.1; JOINED.
REMEL; U23429; AAA91123.1; JOINED.
REMEL; U23429; AAA91123.1; JOINED.
REMEL; U23429; AAA9123.1; JOINED.
REMEL; U23429; AAA9123.1; JOINED.
REMEL; U334254; AAP84362.1; -..
REMEL; D8566; BAA90879.1; -..
REMEL; D86717-NOV-99.
REMEL; D86717-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
Palmitate; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels 1; Gaps
system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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S-palmitoyl cysteine (By similarity).
AGEBFABDA805E610 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 380.5; DB 1; Length 428; Pred. No. 2.6e-33; 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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1 (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47841 MW;
                                                                                                                                                                                                                                                                                                            EMBL; L13605; AAA35659.1; -.
EMBL; L19315; AAA02819.1; -.
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98.8%;
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Best Local Similarity 98.c.
Tocal 79; Conservative
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294 NRIRSNSSAANLMAKKRVIR 313

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                                                                                                                                                                                                                                                                                                          TISSUE=Pancreas;

X. MEDLINE=92212981; Pubmed=1313582;

Mank S.A., Harkins R., Jensen R.T., Shapira H., de Weerth A.,
Slattery T.,
Slattery T.;

Purification, molecular cloning, and functional expression of the
cholecystokinin receptor from rat pancreas.";

Proc. Natl. Acad. Sci. U.S.A. 99:3125-3129(1992).

I proc. Natl. Acad. Sci. U.S.A. 99:3125-3
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

    IISSUE SPECIFICITY: Pancreas and brain.
    SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 111-158; 270-314 AND 392-402
                                           01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
10-0CT-2003 (Rel. 42, Last amotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A42685; A42685.
HSSP; P02699; IR88.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PCRRHODDPSN.
PROSITE; PS00237; G_PCRFN.RECEP_F1_1; 1.
PROSITE; PS00265; G_PROTEIN_RECEP_F1_2; 1.
G-protein, coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
444 AA.
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STANDARD;
                                                                                                                                           CCKAR.
Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                      NCBI TaxID=10116;
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DISULFID
LIPID
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EMBL; AF015963; AAC07949.1; -.
                                                                                                                     389 3
430 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                       CCKR MOUSE
                                               DOMAIN
CARBOHYD
                                                                                             CARBOHYD
DISULFID
LIPID
                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis.
             RANSMEM
                                                                                                                                  SEQUENCE
                                                                       CARBOHYD
                                                                                   CARBOHYD
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  DOMAIN
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                                                                                  TISSUE-Gall bladder, and Pancreas;

X MEDLINE-94106629; PubMed=7916580;
A de Weerth A., Pisegna J.R., Wank S.A.;
A de Weerth A., Pisegna J.R., Wank S.A.;
T "Guinea pig gallbladder and pancreas possess identical CCK-A receptor T subtypes: receptor cloning and expression.";
Am. J. Physiol. 265:Gl116-Gl121(1993).
C - FUNCTION: Receptor for cholecystokinin. Has a 1000 fold affinity for CCK rather than for gastrin. It modulates feeding and dopamine-induced behavior in the central and peripheral nervous system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system (By similarity).
C SUBCELLUAR LOCATION: Integral membrane protein.
C -I-SIMILARITY: Belongs to family 1 of Gprotein coupled receptors.
                                                                      1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                Gaps
                                                                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                               7
                         Length 444;
                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; 151898; 151898.
HSSP: P02699; 1888.
Interpro; 187000276; GPCR_Rhodpsn.
PRINTS: PRO0037; GPCRHJODESN.
PROSTTE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F2; 1.
G-procein coupled receptor; Transmembrane; Glycoprotein; DoMAIN
Lipoprotein; Palmitate.
EXTRACELLULAR (POTENTIAL).
444 AA; 49657 MW; B435BE7505C2FB11 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                       Score 316; DB 1;
Pred. No. 2.1e-26;
8; Mismatches 4;
                                                                                                                                                                                                      430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                  309 LNRIRSSSSAANLIAKKRVIR 329
                                                                                                                   59 ANRIRSNSSAANLMAKKRVIR 79
                       80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S68242; AAB29504.1; -.
                                               Conservative
                                                                                                                                                                                                      STANDARD;
                                 1 Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
116
138
158
179
                                                                                                                                                                                                      CAVPO
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                     Query Match
Best Local {
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lacourse K.A., Lay J.M., Swanberg L.J., Jenkins C., Samuelson L.C.;
"Molecular structure of the mouse CCK-A receptor gene.";
Biochem. Biophys. Ree. Commun. 236:630-635(1997).
-!- FUNCTION: Receptor for Los Receptorin. Has a 1000 fold affinity for CCK rather than for gastrin. It modulates feeding and dopamine-induced behavior in the central and peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second
                                                   EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLESSIC (POTENTIAL).
CYTOPLESSIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                             S-palmitoyl cysteine (By similarity) FC9F5D34032076C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takata Y., Takiguchi S., Takaoka K., Funakoshi A., Miyasaka K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholecystokinin type-A receptor gene and its structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 289.5; DB 1; Length
Pred. No. 1.3e-23;
4; Mismatches 10; Indels
CYTOPLASMIC (POTENTIAL)
                                    6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 RINRIRSSSSTANLMAKKRVIR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ; TISSUE=Liver;
MEDLINE=97254481; PubMed=9099891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ;
MEDLINE=97396148; PubMed=9245702;
                                                                                                                                                                                                                                                                                                                                                                                     48210 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%;
79.3%;
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Best Local Similarity 79.3
Matches 65, Conservative
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Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
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P70031;
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TRANSMEM
DOMAIN
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DOMAIN
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CCKR_XENLA
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Reuben M., Rising L., Prinz C., Hersey S., Sachs G.;
"Cloning and expression of the rabbit gastric CCK-A receptor.";
Biochim. Biophys. Acta 1219:321-327(1994).
-i- FUNCTION: Receptor for cholecystokinin. Has a 1000 fold affinity
for CCK rather than for gastrin. It modulates feeding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).
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R EMBL; AF015959; AAC07949.1; JOINED.
R EMBL; AF015960; AAC07949.1; JOINED.
R EMBL; AF015961; AAC07949.1; JOINED.
R EMBL; D85605; BAAC07949.1; JOINED.
R EMBL; D85605; BAAC07949.1; JOINED.
R EMBL; D85605; BAAC07949.1; JOINED.
R HSSP; P02699; JC5599.
R HSSP; P02699; JC5599.
R MGD; MG1:99478; Cckar.
R InterPro; IPR000276; GPCR_Rhodpsn.
R FRIMTS; PR00237; GPCRHODOPSN.
R PRIMTS; P850227; GPCRHODOPSN.
R PROSITE; P850262; GPROTEIN RECEP_F1_1; 1.
R PROSITE; P850262; GPROTEIN RECEP_F1_2; 1.
R G-protein coupled receptor; Transmembrane; Glycoprotein;
R Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR)
                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
YTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC (P
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10; Mismatches
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Conservative 1
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395
258
265
436 AA;
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Local Si.
63; C
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CARBOHYD
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DISULFID
LIPID
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
dopamine-induced behavior in the central and peripheral nervous system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholecystokinin receptor (CCK-XIR).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-palmitoyl cysteine (By similarity) 089FD10E2B86DB25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.3%; Score 275; DB 1; Length 42 72.5%; Pred. No. 4.6e-22; ive 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interprof. 1PR000276, GPCR Rhodpsn.
Pfam; PF000017, 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
G-protein Coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLOLAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U86601; AAD11547.1; -.
HSSP; P02699; 1F88.
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58; Conservative
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447 AA.

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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR).
                                                                                                                                                                                                                                                                                                                                                     Pisegna J.R., de Weerth A., Huppi K., Wank S.A.; "Molecular cloning of the human brain and gastric cholecystokinin receptor: structure, functional expression and chromosomal
                                                                                                                                            Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=92316795; PubMed=7681836;
Lee Y.-M., Beinborn M., McBride E.W., Lu M., Kolakowski L.F. Jr.,
                                                                                                                                                                                                                                                            "The human brain cholecystokinin-B/gastrin receptor. Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Song I., Brown D.R., Wiltshire R.N., Gantz I., Trent J.M., Yamada T.;
                                                                                                                                                                                                                                                                                                                                                                                                         ochem. Biophys. Res. Commun. 189:296-303(1992)
                                                                                                                                                                                                                                                                                     Biol. Chem. 268:8164-8169(1993).
                                                                                                                                                                                                                                                                                                                                          MEDLINE=93080572; PubMed=1280419;
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                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           characterization.
                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Placenta;
                                                                                                                    CCKBR OR CCKRB
                                                                                                                                                                                                                                                                                                                                                                                             .ocalization."
                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                      HUMAN
                          GASR_HUMAN
                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        "Identification of cholecystokinin-B/gastrin receptor domains that confer high gastrin affinity: utilization of a novel Xenopus laevis cholecystokinin receptor.";
Mol. Pharmacol. 50:416-41(1996).
-!- FUNCTION: Receptor for cholecystokinin. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system. Has high affinity for CCK-8 and low affinities for gastrin-17-1, CCK-4, and unsulfated CCK-8.
                         MEDLINE=96319796; PubMed=8700154;
Schmitz F., Pratt D.S., Wu M.-J., Kolakowski L.F. Jr., Beinborn M.,
                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Brain and stomach.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
HAS EQUAL SIMILARITY TO TYPE A AND B CHOLECYSTOKININ MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-palmitoyl cysteine (By similarity).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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8.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PSO0237; G PROTEIN RECEP F1 1; 1.
PROSITE; PSSO262; G PROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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"The human gastrin/cholecystokinin type B receptor gene: alternative splice donor site in exon 4 generates two variant mRNAs."; Proc. Natl. Acad. Sci. U.S.A. 90:9085-9089(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kopatz S.A., Aronstam R.S., Sharma S.V.;

"CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity.

This receptor mediates its action by association with G proteins
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-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                             MEDLINE=93352657; PubMed=8349705;
Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima Into M., Chiba T., Chibara K.;
Nakata H., Chiba T., Chibara K.;
Functional characterization of a human brain cholecystokinin-B receptor. A trophic effect of cholecystokinin and gastrin.";
J. Biol. Chem. 268:18300-18305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tate S.N., Gray J., Denyer J., Stolz M., Foord S., Lee M.G.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Temporal cortex;
Tate S.N., Gray J., Den;
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BLYQGIKFBASQKKSAKERK----PSTTSSGKYEDSDGCYLK-TRPPRKLELRQLSTGS 55

79

SSRANRIRSNSSAANLMAKKRVIR

320 CTKMDRARINNSEAKLMAKKRVIR 343

Gaps

8

25; Indels

; Pred. No. 8.3e

42.9%;

1 Similarity 42.9 36; Conservative

Local

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244 ELYLGLRFDGDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVG--EDSDGCYVQLPRSR 301

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R GO, 60008887; C:integral to plasma membrane; TAS.

R GO, 600008887; C:integral to plasma membrane; TAS.

R GO, 600008887; C:cholecystckinin receptor activity; TAS.

R GO, 600008935; F:cholecystckinin receptor activity; TAS.

R GO, 600007204; P:cell proliferation; TAS.

R GO, 600007204; P:cell surface receptor linked signal transdu. .; TAS.

R GO, 600007204; P:cell surface receptor linked signal transdu. .; TAS.

R GO, 60007204; P:cell surface receptor linked signal transdu. .; TAS.

R GO, 60007205; P:phosphatidylinositol.4,5-bisphosphate hydro. .; TAS.

R GO, 60007202; P:phosphatidylinositol.4,5-bisphosphate hydro. .; TAS.

R GO, 60007202; P:phosphatidylinositol.4,5-bisphosphate hydro. .; TAS.

R GO, 60007202; P:phospholipase C activation; TAS.

R GO, 60007600; P:sensory perception; TAS.

R InterPro, IPR000276; GPCR_Rhodpsn.

R Ffam; PR00017, TAM. 1, 1.

R RINTS; PR000217; GPRRHODPSN.

R G-prottein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;

R DAMMitate; Polymorphism; D-structure.

R DAMMItate; Polymorphism; D-structure.

R DAMMILL PLOSE POLYMORPHEN RECEPTULALA.

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the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S-palmitoyl cysteine (By similarity).
L -> F (in dbSNP:1805000).
/FTId=VAR 014684.
V -> I (in dbSNP:1805002).
/FTId=VAR 014685.
R -> H (in dbSNP:1805004).
/FTId=VAR 014686.
R -> Q (in dbSNP:1805001).
/FTId=VAR 014686.
A -> P (in REP: 5).
L -> V (IN REF: 5).
L -> V (IN REF: 5).
My; BAEEFAD4CIF85915 CRC64;
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28.6%; Score 112; DB 1; Length 447;
Best Local Similarity 33.7%; Pred. No. 0.00012;
Matches 34; Conservative 14; Mismatches 19; Indels 34;
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CYTOPLASNIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR.
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                       EMBL; L08112; AAA35657.1; --
EMBL; L04473; AAA35660.1; --
EMBL; L10822; AAC37528.1; --
EMBL; D13305; BAA02564.1; --
EMBL; L07746; AAA91831.1; --
EMBL; AY32551; AAP84364.1; --
EMBL; AY32551; AAP84364.1; --
PDB; L147; 28.7AN-03.
Genew; HONC:1571; CCKBR.
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447 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blochem. Biophye. Res. Commun. 272:837-842(2000).

-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELJULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ;
MEDLINE=20318371; PubWed=10860839;
Lay J.M., Jenkins C., Friis-Hansen L., Samuelson L.C.;
"Structure and developmental expression of the mouse CCK-B receptor
                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:99479; Cckbr.
InterPro; IPR000276; GPCR_Rhodpsn.
PFam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                   Kopin A.S.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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CYTOPLASMIC (POTENTIAL).
42 PPRKLELROLST --- GSSSRANRIRSNSSAANLMAKKRVIR
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EMBL; AF264178; AAG09801.1; --
EMBL; AF264177; AAG09801.1; JOINED.
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P56481;
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                                                                                                                                                                                  -----KPSTTSSGKYEDSDGCYL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92412082; PubMed=1530611;
Nakata H., Matsui T., Ito M., Taniguchi T., Naribayashi Y., Arima N.,
Nakamura A., Kinoshita Y., Chihara K., Hosoda S., Chiba T.;
"Cloning and characterization of gastrin receptor from ECL carcinoid
tumor of Mastomys natalensis.";
Biochem Biophys Res. Commun. 187:1151-1157(1992).
-!- FUNCTION: Receptor for gastrin and cholecystckinin. The CKK-B
receptors occur throughout the central nervous system where they
modulate anxiety, analgesia, arousal, and neuroleptic activity.
This receptor mediates its action by association with G proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Stomach and brain. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                       Praomys natalensis (African soft-furred rat) (Mastomys natalensis)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that activate a phosphatidylinositol-calcium second messenger
         CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                           S-palmitoyl cysteine (By similarity) DFD21432C323405C CRC64;
                                                                                                                                           28;
                                                                                                                Length 453;
                                                                                                                 Score Lus,
Pred. No. 0.0011;
Pred. Terrines 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00001; 7tm 1; 1. —
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS050252; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                      : | :||:||:||:|
QL-PRSRLEMTTLTTPTTGPGPGPRPNQ--AKLLAKKRVVR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                       39 KTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                450 AA
 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (POTENTIAL)
                                                                                                                                                                     2 ELYQGIKFEASQKKSAKER------
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Pfam; PF00001; 7tm 1; 1.
                                                                                                                                           16;
                                                                                         49171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D12817; BAA02250.1; -.
                                                                                                                 26.3%;
                                                                                                                               29.78;
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein, Palmitate.
DOMAIN 1 57
                                                                           414
453 AA;
                                                                                                                               Local Similarity
les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mastomys.
NCBI_TaxID=10112;
                                                                                                                                                                                                                                                                                                                GASR PRANA
                                                CARBOHYD
DISULFID
                                                                           LIPID
SEQUENCE
TRANSMEM
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                           CARBOHYD
                                     CARBOHYD
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                       RESULT 9
GASR_PRANA
                                                                                                                                                                                                                                                                                                                                                                                            CCKBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EDSDGCYLKTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wank S.A., Pisegna J.R., de Weerth A.;
"Brain and gastrointestinal cholecystokinin receptor family:
structure and functional expression.";
Proc. Natl. Acad. Sci. U.S.A. 89:861-8695(1992).
-:- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B
receptors occur throughout the central nervous system where they
modulate anxiety, analgesia, arousal, and neuroleptic activity.
This receptor mediates its action by association with G proteins
that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Parietal cells, pancreas, brain and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplastic tissues.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
10-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                 S-palmitoyl cysteine (By similarity)
EF13BA8B5FAA857A CRC64;
                                                                                                                                                                                                                                                                                               (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                       6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POT
                          2 (POTENTIAL).
EXTRACELULAR (POTENTIAL)
                                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 PRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 RSRLEMITLITPIPGPG---LASANQAKLLAKKRVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 101.5; DB 28.9%; Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 AA
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TISSUE=Brain;
MEDLINE=92409582; PubMed=1528881;
                                                                                                                                                                                                                                                                                                                                                                                                                           48755 MW;
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nes 28; Conservative
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336
3376
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Matches
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GASR_RAT
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STANDARD;
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362
380
401
454
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454 AA;
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RABIT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 98.5; DB 1; Leus-...
Pred. No. 0.0033;
....has 29; Indels 27;
                                                                               PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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006D811A6AA065C6 CRC64;
                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ELYQGIKFEASQKKSAKER------
               PIR; A46195; A46195.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P79266,
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
10-OCT-2003 (Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * Query Match
• Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ELYQGIKFEASQKKSAKER-----KPSTTSSGKY---------EDSDGCYL-- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Gaps
                        .i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-palmitoyl cysteine (By similarity) A2846A580508ABA6 CRC64;
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101-NOV-1995 (Rel. 32, Created)

101-NOV-1995 (Rel. 32, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Gastrin/cholecystokinin type B receptor (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TY (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 RSRP--ALEMSALTAPTPGPGSGTR------PAQAKLLAKKVVR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                        LIGENTO, IPRO0015, GPCR_Rhodpen.

Fiden, PF00001, PF000015

PERINTS, PR00237; GPCRRHODDESN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation.

DOMAIN.

EXTRACELULAR FOOTENMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 KTRPPRKLELRQLST-----GSSSRANRIRSNSSAANLMAKKRVIR
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7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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-! - SUBCELLULAR LOCATION: Integral membrane protein
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Liver;
MEDLINE-94324990; PubMed=8048969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48781 MW;
                                                                                                                                                                                                                                                                                                                               EMBL; S83090; AAB46896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 29.2%
Matches 31; Conservative
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10-OCT-2003 (Rel. 42, Last annotation update)
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DISULFID
LIPID
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TRANSMEM
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KPSTTSSGKYEDSDGCYL- 38
Blandizzi C., Song I., Yamada T.;
"Molecular cloning and structural analysis of the rabbit gastrin/CCKB
                                        FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proceins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Gaps
                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                    activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-palmitoyl cysteine (By similarity)
E0716FCC1DB38870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91.5; DB 1; Length 452;
Pred. No. 0.018;
5; Mismatches 27; Indels 3:
                                                                                                                                                                                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 LPRSRP--ALELSALTAPISGPGPGPR--PAQAKLLAKKRVVR 338
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                               Biophys. Res. Commun. 202:947-953(1994).
                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GASR_CANFA STANDARD; PRT; 453 AA P30.52; 046376; 01-ARR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                     InterPro; IPR000276; GPCR Rhodpsn.
                                                                                                                                                                                                                             EMBL, L31548; AAA31194.1; -.
EMBL, L31547; AAA31194.1; JOINED.
PIR: JC2459; JC2459.
HSSP; P02699; 1F88.
                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48730 MW;
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CARBOHYD
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                                Biochem
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ID GASR_CI
AC P30552
DT 01-APR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Song I., Blandizzi C., Brown D.R., Kang D.H., Todisco A., Delvalle J., del Tacca M., Owyang C., Yamada T., "Molecular cloning and structural analysis of the canine gastrin/CCK-B
                                                                                                                                                                                                                                                                                                                                Kopin A.S., Lee Y. M., McBride E.W., Miller L.J., Lu M., Lin H.Y., Kolakowski L.F. Jr., Beinborn M.; "Expression cloning and characterization of the canine parietal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICITY: Parietal cells, pancreas, brain and various neoplastic tissues.
-:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
S-palmitoyl cysteine (By similarity).
                            Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation.
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 89:3605-3609(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Parietal cell;
MEDLINE-92228835; PubMed=1373504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AD001537; AAB87706.1; -. PIR; S32817; S32817.
HSSP; P02699; 1F88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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131
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170
189
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residues.
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                                                                                   -----KPSTTSSGKYEDSDGCYLK-T 40
                                              Gaps
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=9936226; PubMed=1043361;
Villard L., Fontes M., Ewbank J.J.;
"Characterization of xnp-1, a Caenorhabditis elegans gene similar to the human XNP/ATR-X gene.";
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                 28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transcriptional regulator ATRX homolog (X-linked nuclear protein-1).
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Bristol N2;
Fulton R., Wohldmann P.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could be a global transcriptional regulator. Modifies gene expression by affecting chromatin (Potential).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00690; DEAH ATP HELICASE; FALSE NEG.
DNA repair; Hydrolase; Helīcase; Nuclear protein; ATP-binding;
DNA-binding.
                    21.9%; Score 85.5; DB 1; Length 453; 28.3%; Pred. No. 0.08; ive 14; Mismatches 32; Indels 2!
453 AA; 48518 MW; 0FAEB7B994B44E1F CRC64;
                                                                                                                                    303 RSRQTLELSALTAPTPGPGGGPRPYQ--AKLLAKKRVVR 339
                                                                                                               79
                                                                                                              41 RPPRKLELROLSTGSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                             1359 AA.
                                                                  ELYQGIKFEASQKKSAKER------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTEN DEAH BOX. POLY-ASP. POLY-GLU. POLY-IXS. POLY-IXS. POLY-IXS.
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WormNep, B0041.7, CE17314.

InterPro; IPR001410; DEAD.

InterPro; IPR001650; Helicase_C.

InterPro; IPR00330; SNF2 N.

Pfam; PF00271; helicase_C; 1.

Pfam; PF00176; SNF2_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF134186; AAD55361.1; -. EMBL; AF000196; AAC24256.1; -.
                                           28; Conservative
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00487; DEXDC; 1
SMART; SM00490; HELICC;
                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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639
70
272
281
375
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                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                               XNP-1 OR B0041.7
                                                                                                                                                                                            ATRX CAEEL 5
09U7E0; 002061;
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8 KFEASQKKSAKERKPSTTSSGKYEDSD-GCYLKTRPPRKLELRQLSTGSSSRA---NRIR 63
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J. Biol. Chem. 265:3012-3016(1990).
-!- FUNCTION: Pancreastatin strongly inhibits glucose induced insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of porcine chromogranin A messenger RNA demonstrates chromogranin A can serve as the precursor for the biologically active
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93345362; PubMed=8344192;
Fasciotto B.H., Trauss C.A., Greeley G.H., Cohn D.V.;
"Parastathin (porcine chromogranin A347-419), a novel chromogranin A-derived peptide, inhibits parathyroid cell secretion.";
Endocrinology 133:461-466(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CMGA_PIG STANDARD; PRT; 446 AA.
P04404;
20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chromogranin A precursor (CgA) [Contains: Pancreastatin; Parastatin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Parastatin inhibits low calcium-stimulated parathyroid cell secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granules.
PTM: Oglycosylated.
PTM: Parathyroid CHGA is sulfated on tyrosine residues, whereas adrenal CHGA seems to be mainly sulfated on oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88196011; PubMed=2834189;
Iacangelo A.L., Fischer-Colbrie R., Koller K.J., Brownstein M.J.,
Eiden L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Pancreastatin, a novel pancreatic peptide that inhibits insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
                                                                                                                                                                                                                          4
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Gorr S.U., Cohn D.V.;
"Secretion of sulfated and nonsulfated forms of parathyroid
                                                                                                                                                          DB 1; Length 1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87065127; PubMed=3537810;
Tatemoto K., Bfendie S., Mutt V., Makk G., Feistner G.J.,
Barchas J.D.;
                                                                                                                                                                                                                       34; Indels
603 608 POLY-LYS.
859 862 POLY-LYS.
479 479 C -> F (IN REF. 2).
1359 AA; 156191 MW; BB4342547D4F4E64 CRC64;
                                                                                                                                                                                                                    12; Mismatches
                                                                                                                                                       18.7%; Score 73; 31.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 122:2339-2341(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  release from the pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 KSKKNKEKSVKKR 179
                                                                                                                                                                                                                                                                                                                                                                                                        64 SNSSAANLMAKKR 76
                                                                                                                                                                                                                    23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 324:476-478(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreastatin.
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 256-304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 363-377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
MISCELLANEOUS: Binds calcium with a low-affinity.
SIMILARITY: Belongs to the chromogranin / secretogranin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARASTATIN.
BY SIMILARITY.
AMIDATION (G-305 PROVIDE AMIDE GROUP).
D9801F9596D39CD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Signal; Amidation; Glycoprotein; Sulfation; Calcium-binding.
NON TER 1 1 1 SIGNAL <1 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.3%; Score 71.5; DB 1; Length 446; 32.5%; Pred. No. 2.5;
                                                                                                                                    and
                                                                                                                 use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMOGRANIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PANCREASTATIN.
WE-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 2.5;
10; Mismatches
                                                                                                                                                                                                                                 HSSP; P05059; ICFK.
GlycoSuiteDB; P04404; -.
Interpro; IPR001919; Chromogranin_AB.
InterPro; IPR001990; Granin.
Pfam; PF01271; Granin; 1.
PRINTS; PR00659; CHROMOGRAIN.
PROSITE; PS00422; GRANINS_1; 1.
PROSITE; PS00423; GRANINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 49323 MW;
                                                                                                                                                                                                  EMBL; M20926; AAA31016.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.5'
Matches 25; Conservative
                                                                                                                                                                                                                 , A32284; A32284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 AA;
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MOD RES
SEQUENCE
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Search completed: October 1, 2004, 16:36:59 Job time: 11 secs

| |:| :||| 173 ----STHPLASLPSKKR 185

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60 NRIRSNSSAANLMAKKR 76

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2 BLYQGIKFEASQKKSAKERKPSTISSGKYEDSDGC--YLKTRPPRKLELRQLSTGSSSRA 59

7; Gaps

35; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-841-091B-20 391 1 LELYQGIKFEASQKKSAKER.....NRIRSNSSAANLMAKKRVIR 79

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 Total number of hits satisfying chosen parameters: 1017041 segs, 315518202 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_lungi:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mcmal:\*
sp\_ncanelle:\*
sp\_organelle:\* SPTREMBL 25:\* Database :

plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					SOUTHERED	
Result		Oùerv				
No.	Score	Match	Match Length DB	DB	ID	Description
1	284.5	72.8	436	1	Q9DBV6	Q9dbv6 mus musculu
~	284.5	72.8	436	11	Q8VCC7	OBvcc7 mus musculu
m	138.5	35.4	436	13	Q7T1P8	O7t1p8 gallus gall
4	112	28.6	90	4	Q9UBV1	Ogubvi homo sapien
S	112	28.6	396	4	075824	075824 homo sapien
9	112	28.6	396	4	Q92492	Q92492 homo sapien
7	112	28.6	447	4	Q16144	homod
<b>ω</b>	103	26.3	453	11	QBBKF6	Osbkf6 mus musculu
σ	101.5	26.0	296	11	P90333	P90333 praomys nat
10	101.5	26.0	316	11	P89000	
11	101.5	26.0	450	11	P89005	P89005 praomys nat
12	98.5	25.2	381	11	Q63095	
13	92.5	23.7	516	4	Q9NYK7	O9nyk7 homo sapien
14	92.5	23.7	516	4,	931960	O961c6 homo sapten
15	81.5	20.8	258	~	93306	0933q6 shiqella fl
16	74	18.9	225	Ŋ	Q9V6Q2	Q9v6q2 drosophila

O7yud5 drosophila				P91959 psammechinu			Q984j4 streptococc			Q8nix6 neurospora	Q9d029 mus musculu	O14562 homo sapien	O9nkyl drosophila	Q868me dugesia jap	Q9le81 arabidopsis		Q7xd45 oryza sativ	Q28708 oryctolagus	Q9nah6 caenorhabdi	Q8eyk4 leptospira	Q86iy3 dictyosteli	O9vi42 drosophila	OBriss mus musculu	Q8bka3 mus musculu	O9zwbl arabidopsis	Q9w0h4 drosophila	Q18264 caenorhabdi	Q8utv3 human immun
Q7YUDS	Q7YUD4	Q81G74	QBMVN1	P91959	045614	6НХХ6Ф	Q9S4J4	959X6Q	036X6Q	9XIN8Ö	090029	014562	Q9NKY1	Q868M6	Q9LE81	Q9FWV2	Q7XD45	028708	Q9NAH6	Q8EYK4	Q861Y3	Q9VJ42	Q8R1S5	QBBKA3	Q9ZWB1	Q9W0H4	Q18264	QBUTV3
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225	225	585	213	299	3102	91	229	246	435	204	309	533	1045	1076	1168	986	988	533	580	695	509	1377	120	608	672	1150	1715	134
18.9	18.9	18.7	18.3	18.3	18.3	18.2	18.2	18.2	18.2	18.0	18.0	18.0	18.0	17.9	17.9	17.8	17.8	17.5	17.5	17.5	17.4	17.4	17.3	17.3	17.3	17.3	17.3	17.1
74	74	73	71.5	71.5	71.5	71	71	71	71	70.5	70.5	70.5	70.5	70	70	69.5	69.5	68.5	68.5	68.5	68	68	67.5	67.5	67.5	67.5	67.5	67
17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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251 ELYRGIRFELDIKGEAAAQR-STEPLPTCDEGDGCYLQLSRPGGALELRALG-AAGAQQE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=94036800; PubMed=8221657; Sethi T., Herget T., Wu S.V., Walsh J.H., Rozengurt E.; Sethi T., Herget T., Wu S.V., Walsh J.H., Rozengurt E.; "CCKA and CCKB receptors are expressed in small cell lung cancer lines and mediate Ca2+ mobilization and clonal growth."; Cancer Res. 53:5208-5213(1993). SEQUENCE 90 AA; 9547 MW; 336A0F09E7C0857B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ELYQGIKFEASQKKSAKER----KTR----KPSTTSSGKYEDSDGCYL---KTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELYQGIKPEASQKKSAKERKPSTTSSGKYEDSDGCYLK-TRPPRKLELRQLSTGSSSRAN
                                                                                                               Gallus gallus (Chickén).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae; Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
28.6%; Score 112; DB 4; Length 90;
Best Local Similarity 33.7%; Pred. No. 2.4e-05;
Matches 34; Conservative 14; Mismatches 19; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Cholecystokinin B/gastrin receptor (Fragment).
Cholecystokinin B/gastrin receptor (Fragment).
Eukaryotain (Hunan).
Eukaryotai Metakuan).
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 436;
                                                                                                                                                                                                                                                                 Nilsson I.B.M., Monstein H.J., Svensson S.P.S.; "Molecular cloning and characterization of a chicken brain cholecystokinin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Match 35.4%; Score 138.5; DB 13; Length Local Similarity 45.6%; Pred. No. 1.2e-07; les 36; Conservative 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
Nilsson I.B.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJ489483; CAD33800.1; -.
                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 AA; 47749 MW; 429C1D7AFE774DC5 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RIRSNSSAANLMAKKRVIR 79
                                                                             Cholecystokinin receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                         NCBI_TaxID=9031;
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01-MAY-2000 (
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                             Gallus
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                                                                                                                                                                                                                                                                                                                                     234 LELYQCIKFDASQKKSAKEKRLSSGGGGGGSSSSRYEDSDGCYLQKSRPPRKLELQQLS 293
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HSSP; P02699; 1F88.

MGD; MGI:99478; CcKar.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IFR000276; GPCR_Rhodpsn.

PRINTS; PR00237; GPCR_Rhodpsn.

PRINTS; P800237; GPROTEIN_RECEP_F1 1; 1.

PROSITE; PS00262; GPROTEIN_RECEP_F1 2; 1.

SEQUENCE 436 AA; 48446 MW; 4984AD57F080F08A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LELYQGIKFEASOKKSAKERKPST-----TSSGKYEDSDGCYL-KTRPPRKLELRQLS
                                                                                                                                                                                                                                                                                                             1 LELYQGIKFEASQKKSAKERKPST-----TSSGKYEDSDGCYL-KTRPPRKLELRQLS
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
ز
                                                                                                                                                                                                                                 72.8%; Score 284.5; DB 11; Length 436; 71.6%; Pred. No. 1.5e-24; ive 10; Mismatches 6; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.8%; Score 284.5; DB 11; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20%.)
Pred. No. 1.5e-24;
.....rorches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 AA; 48396 MW; FD35D8453B792F79 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                               294 TSSSGGRINRIRSSGSAANLIAKKRVIR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 TGSS-SRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                           53 TGSS-SRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.6%;
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01-JUN-2003 (TrEMBLrel. 24,
Cholecystokinin A receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 71.63
Matches 63; Conservative
                                                                                                                                                                                                                                                                           63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
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RESULT 3 Q7T1P8 ID Q7T1P8

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TISSUB-LUNG;
MEDLINE=95151633; PubMed=7848914;
MEDLINE=95151633; PubMed=7848914;
Ito M., Iwata N., Taniguchi T., Murayama T., Chihara K., Matsui T.;
Ito M., Iwata N., Taniguchi T., Murayama T., Chihara K., Matsui T.;
"Functional characterization of two cholecystokinin-B/gastrin receptor isoforms: a preferential splice donor site in the human receptor
                                                        TISSUE=Lung;
MEDLINE=94038108; PubMed=8222757;
Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
"Localization of the human cholecystokinin-B/gastrin receptor (CCKBR) to chromosome 11p15.5-->p15.4 by fluorescence in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 AA
                                                                                                                                                                       Cytogenet. Cell Genet. 65:184-185(1994)
J. Biol. Chem. 268:18300-18305(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 16-26 FROM N.A.
MEDLINE=95194412; Pubmed=7887934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D21219; BAA04759.1; -. EMBL; S76072; AAB33740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholecystokinin B receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AA;
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyake A.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cholecystokinin-B receptor/gastrin receptor (CCK-B gastrin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Lung;
MEDLINE-9335267; PubMed-8349705;
Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima I.Nakata H., Chiba T., Chibara F., Chibara H., Chiba T., Chibara F., "Functional characterization of a human brain cholecystokinin-B
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                           MEDLINE=99087707; PubMed=9872672;
0'Briant K.C., Ali S.Y., Weier H.U.G., Bepler G.;
"An 84-kilobase physical map and repeat polymorphisms of the gastrin/cholecystokinin brain receptor region at the junction of chromosome segments llpl5.4 and 15.5.";
chromosome Res. 6.415-418(1998).
EMBL; AF074029; AAC27510.1;
EMBL; AF074025; AAC27510.1;
PIR; 165231; 165231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional characterization of a human brain cholecystokinin-B receptor. A trophic effect of cholecystokinin and gastrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; F:G-protein coupled receptor protein signalin.
InterPro; IPR00207; GPCR_Rhodopsn.
PRINTS; PR00237; GPCRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 112; DB 4; Length 396; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 AA; 43286 MW; 54BE9A8D0257C4E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPRKLELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Gastrin\cholecystokinin brain receptor (Fragment).
                                                          396 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00237; GPROTEIN RECEP F1 1; 1. PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
                                                                                                 Created)
                                                        PRT;
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                                                          PRELIMINARY;
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                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoform) (Fragment).
CCKBR OR CCK-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                              01-NOV-1998
01-NOV-1998
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Q92492;
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Matches

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193 BLYLGLRFDGDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVG--EDSDGCYVQLPRSR 250
                                                                                                                                                                                                                                                                     GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001386; P:G-protein coupled receptor protein signalin. .; IEA.
GO; GO:0001386; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPRO00276; GPCR.Rhodpsn.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPCTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
NON_TER 396
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TISSUE=Brain;
MEDLINE=94241526; PubMed=8185170;
Herget T., Sethi T., Wu S.V., Walsh J.H., Rozengurt E.;
Herget T., Sethi Btimulates Ca2+ mobilization and clonal growth in small cell lung cancer through CCKA and CCKB/gastrin receptors.";
"A fruncated isoform of human CCK-B/gastrin receptor generated by alternative usage of a novel exon."; Biochem. Biophys. Res. Commun. 208:230-237(1995).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43252 MW; A25DD5597CA903C0 CRC64;
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Last annotation update)
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28.6%; Score 112; DB 4;
Best Local Similarity 33.7%; Pred. No. 0.00012;
Matches 34; Conservative 14; Mismatches 19
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302 QL-PRSRLEMTTLTTPTTGPGPGPRPNQ--AKLLAKKRVVR 339
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PRINTS; PR00237; GPCRRHODOPSN.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   Mastomys.
NCBI_TaxID=10112;
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NON TER
SEQUENCE
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Matches
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                                                                    RESULT
P90333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 ELYLGLRFDGDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGK--DSDGCYVQLPRSR 301
                                                                                        GO, GO:0016021, C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO:0007186; F:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
PFam; PF00001; 7tm_1; 1.
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EMBL, AKO53307; BAG15337.1; -.

EMBL, AKO53307; BAG15337.1; -.

EMBL, AKO53307; Cokbr.

GO; GO:0016584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IPR000276; GPGR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ELYQGIKFEASOKKSAKER-------KPSTTSSGKYEDSDGCYL---KTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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                                                                                                                                                                                                                                                                                                                                                                           Match 28.6%; Score 112; DB 4; Length 447; Local Similarity 33.7%; Pred. No. 0.00014; es 34; Conservative 14; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0237; GPCKRHODOPSN.
PROSITE; PS00227; G-PROTEIN RECEP FI_1; 1.
SEQUENCE + 950262; G-PROTEIN_RECEP_FI_2; 1.
SEQUENCE + 453 AA; - 49143 MW; FCEO7980A678250A CRC64;
                                                                                                                                                                                                                                                                                                                              447 AA; 48418 MW; E3DAAESEE1F0FB99 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Gastrin/cholecystokinin type B receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 AA
                                                                                                                                                                                                      PEam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
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MEDLINE=22354683; PubMed=12466851;
                   EMBL; S70057; AAB30766.2; -. PIR; 165231; 165231.
HSSP; P02699; 1F88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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01-OCT-2003
                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ELYQGIKFEASQKKSAKER-----KPSTTSSGKY------BDSDGCYLKTRP
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Gastrin/cholecystokinin receptor (Fragment).
Fracourys natalensis (African soft-furred rat) (Mastomys natalensis)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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The Anadis na Anatlensis (African Soft-Uurred rat) (Mastomys natalensis)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:-protein compled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Luque E.A., Tang L.H., Modlin I.M.;
"Gastrin receptors in Mastomys natalensis.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U49833, ABB41676.1; -
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296 296 296 MW; 320FF55B102DB4C2 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.0%; Score 101.5; DB: 28.9%; Pred. No. 0.0015; iive 18; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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CCK(B) receptor (CCK2 receptor) (Fragment).
                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 BLYQGIKFEASQKKSAKER-----KPSTISSGKY------EDSDGCYLKTRP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
PF00001; 7tm_1; 1.
                                                                                                                                      2 ELYQGIKFEASQKKSAKER-----KPSTTSSGKY------EDSDGCYLKTRP
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Gastrin/cholecystokinin-B receptor (Fragment).
Praomys natalensis (African Soft-furred rat) (Mastomys natalensis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucleoscomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                            Length 316;
                                                                                                                  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Lugue E.A., Tang L.H., Modlin I.W.;
"Gastrin receptor expression in Mastomys natalensis.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                            1 1
316 316
316 AA: 34726 MW; FOD346BAFC6C19E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 AA; 48792 MW; 333F4C368B7A0A97 CRC64;
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Last sequence update)
Last annotation update)
                                                                                           DB 11;
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303 RSRLEMITLITPTPGPG---LASANQAKLLAKKRVVR 336
                                                                                                                                                                                  43 PRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
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                                                                                         26.0%; Score 101.5; DB : 28.9%; Pred. No. 0.0016; Live 18; Mismatches 2
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PSO0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                 28; Conservative
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                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10112;
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01-NOV-1996 (
01-NOV-1996 (
01-OCT-2003 (
                                   Receptor.
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Q63095
ID Q6309
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DT 01-NO
DT 01-OC
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"Genetic variations in CCK2 receptor in PVG hooded and Sprague-Dawley rats and its mRNA expression on cat exposure.";

If and its mRNA expression on cat exposure.";

If Behav. Neurosci. 117:385-390(2003).

If EMBL; X79209; CAA55798.1;

If REMBL; X79209; CAA55798.1;

If S48049; S48049.

If GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

R PRINTS; PR00237; G PROTEIN RECEP FI 1; 1.

R PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
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                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                MEDLINE=95016646; PubMed=7931273;
Jagerschmidt A., Popovici T., O'Donohue M., Roques B.P.;
"Identification and characterization of various cholecystokinin B receptor mRNA forms in rat brain tissue and partial determination the cholecystokin B receptor gene structure.";
J. Neurochem. 63:1199-1206(1994).
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Hellmich M.R., Rui X.L., Hellmich H.L., Fleming R.Y.D., Evers B.M. Townsend C.M. Jr.;
Townsend C.M. Jr.;
"Human Colorectal Cancers Express a Constitutively Active Cholecystokinin-B/Gastrin Receptor That Stimulates Cell Growth.";
J. BJOL. Chem. 275:32122-32128 (2000).
EMBL; AF239668; AAF67174.1;
PIR; I65231; I65231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22594138; PubMed=12708535;
Wang H., Zhu Y.Z., Farook J.M., Moochhala S., Teo A.L., Lee L.K.,
Wong P.T.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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381 AA; 41667 MW; DDCB40806A604A4D CRC64;
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Last sequence update)
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25.2%; Score Surs, Conset Local Similarity 30.0%; Pred. No. 0.004

Matches 30; Conservative 14; Mismatches
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Rattus norvegicus (Rat).
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高级 医红色

5

Gaps

17;

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349 RPETGAVG--EDSDGCYVQLPRSRP--ALELTALTAPGPGSGSRPTQ-----AKLLAK 397
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                                                                       / Match 23.7%; Score 92.5; DB 4; Length 516; Local Similarity 43.1%; Pred. No. 0.03; les 28; Conservative 9; Mismatches 11; Indels 1
516 AA; 55841 MW; EC7EB8505C9A8F0D CRC64;
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       SEQUENCE
                                                                               Query Match
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Int. '0 Mol. Med. 10:689-694(2002).

EMBL; AX029770; AAK38351.1; -.

EMBL; AF41129; AAN32882.1; -.

R MBL; AF41129; AAN32882.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001584; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin. . .; IEA.

R GO; GO:0001584; F:rhodopsin-like receptor protein signalin. . .; IEA.

R GO; GO:0001576; GPCR_Rhodopsn.

R PRINTS; PRO0001; 7cm 1; 1.

R PRINTS; PRO0237; GPCRHODOPSN.

R PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

R RCSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 RPETGAVG--EDSDGCYVQLPRSRP--ALELTALTAPGPGSGSRPTQ-----AKLLAK 397
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                                                                                                                  .; ISS.
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                               GG; GG:0005887; C:integral to plasma membrane; ISS.
GG; GG:0004951; F:cholecystokinin receptor activity; ISS.
GG; GG:00046951; F:cholecystokinin receptor activity; ISS.
GG; GG:0004435; F:phosphatidylinositol 3-kinase regulator act. . .; I
GG; GG:0004435; F:phosphotinositide phospholipase C activity; ISS.
GG; GG:0000435; F:phosphotinositide phospholipase C activity; ISS.
GG; GG:0007504; P:cytosolic calcium ion concentration elevation; ISS.
GG; GG:0007586; P:digestion; ISS.
GG; GG:0007202; P:phospholipase C activation; ISS.
GG; GG:0007609; P:phospholipase C activation of cell proliferation; ISS.
GG; GG:0007600; P:sensory perception; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Characterization of the CCK-C (cancer) receptor in human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Scheber E., Schmidt W.E.; Schmitz F., Schrader H., Stueber E., Schmidt W.E.; "Identification of CCK-B/gastrin receptor splice variants in human peripheral blood mononuclear cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22216923; PubMed=12429993;
Smith J.P., Verderame M.F., McLaughlin P., Martenis M., Ballard
Zagon I.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5; DB 4; Length 516;
Pred. No. 0.03;
9; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CCK-B/gastrin receptor variant (Cholecystokinin-C receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral blood mononuclear cells.";
Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 AA; 55857 MW; 02291E30D9B7971C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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PRINTS; PR00237; GPCRRHODOPSN
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les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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398 KRVVR 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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10261CG
1026
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J. Bacteriol. 183:3958-3966 (2001).
EMBL; AF281292; AAK67308-1; -..
EMBL; AF281291; AAK67308-1; -..
EMBL; AF281291; AAK67306-1; -..
EMBL; AF281291; CABC Company Cterm; J. SEQUENCE 258 AA; 28689 WW; 55A5504B909C32DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 EASOKKSAKERKPSTTSSG-----KYEDSDGCYLKTRPPRKLELRQLSTGSSSRANRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.8%; Score 81.5; DB 2; Length 258; 29.3%; Pred. No. 0.26; tive 14; Mismatches 28; Indels 1:
                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 1, 2004, 16:37:44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES=S.flexneri, and E.coli;
MEDLINE=21289081; PubMed=11395459;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Shigella
NCBI_TaxID=623, 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 SSNAAPQALVESSRI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 RSNSSAANLMAKKRV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smajs D., Weinstock G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri, and Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                    398 KRVVR 402
75 KRVIR 79
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